

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 07:17:45 ; Search time 1411 Seconds
(without alignments)
15357.591 Million cell updates/sec

Title: US-10-067-977-1
Perfect score: 1338
Sequence: 1 atggggagatgcaggcgc.....ccacggactcttctctga 1338

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
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2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
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13: gb_est4:*
14: gb_est5:*
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23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	809.8	60.5	895 14	BQ925372
2	808.4	60.4	1072 13	BM455819
3	795.8	59.5	887 13	BI259163
4	771	57.6	1006 13	BM542149
5	757.2	56.6	888 14	BQ425968
6	751.6	56.2	938 14	BQ936977

7	746.4	55.8	982 14	BQ934765
8	730.2	54.6	851 13	BI764996
9	712.8	53.3	741 9	AUI134278
10	709.8	53.0	736 12	BG575325
11	707.4	52.9	811 9	AL530006
12	707.4	52.8	969 13	BI333256
13	702.6	52.5	1070 13	BM460788
14	701	52.4	940 14	BQ714990
15	698.4	52.2	845 12	BG762418
16	697.8	52.2	849 14	BQ428408
17	695	51.9	1033 14	BQ051239
18	684.8	51.2	910 13	BI256003
19	675.2	50.5	923 13	BI551358
20	664.4	50.2	799 9	AU080100
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22	651.8	48.7	860 9	AUI18064
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24	630	47.1	933 14	BQ888361
25	621.4	46.4	868 10	BE304666
26	621	46.4	898 14	BQ687393
27	620.4	46.4	909 13	BM006359
28	620.2	46.4	860 12	BF689365
29	620	46.3	997 14	BQ691213
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31	616.2	46.1	873 13	BI651188
32	611.8	45.7	782 9	AUI135766
33	607.4	45.4	953 13	BI851305
34	602.8	45.1	915 14	BQ959701
35	601.6	45.0	700 10	BE547715
36	601.2	44.9	908 13	BM015162
37	601	44.9	758 13	BI838931
38	598.8	44.8	735 9	AL598724
39	597	44.6	765 12	BG763506
40	595.2	44.5	906 12	BG715428
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45	584.6	43.7	825 13	BI670405

ALIGNMENTS

RESULT 1
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LOCUS BQ925372 895 bp mRNA linear EST 20-AUG-2002
DEFINITION AGENCOURT_8732778 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:6455661
5', mRNA sequence.
ACCESSION BQ925372
VERSION BQ925372.1 GI:22340403
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 895)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2634 row: k column: 22
High quality sequence stop: 685.
Location/Qualifiers
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BI333256 602996596
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BQ687393 AGENCOURT
BM006359 6031615058
BF689365 602186706
BQ691213 AGENCOURT
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BI651188 603297667
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BI851305 603377887
BQ959701 AGENCOURT
BE547715 601076321
BM015162 603641156
BI838931 603085242
AL598724 DKFZP313C
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/lab_host="DH10B (phage-resistant)"
/notes="Organ: lung; Vector: pOTB7; Site 1: EcoRI; Site 2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT: 235 a 233 c 215 g 211 t 1 others
ORIGIN

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Query Match 60.5%; Score 809.8; DB 14; Length 895;
Best Local Similarity 97.5%; Pred. No. 1.3e-218;
Matches 844; Conservative 0; Mismatches 18; Indels 4; Gaps 2;

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QY 61 CACAAAAGAGGCGGAGGCGCGAGAAAGAGGAGGAGTCTTCTGCTGAGCGGACTGGCT 120
DB 75 CACAAAAGAGGCGGAGGCGCGAGAAAGAGGAGGAGTCTTCTGCTGAGCGGACTGGCT 134
QY 121 TTCATGAAGCAGAGGAGGATGGGTCTGAACGACTTTATTTCAGAGAGTTGCCAATACTCC 180
DB 135 TTCATGAAGCAGAGGAGGATGGGTCTGAACGACTTTATTTCAGAGAGTTGCCAATACTCC 194
QY 181 TATGCATGCAACACCCCTGAAGTTCAGTCCATCTTGAAGATCTCCCACTCAGGAGCCT 240
DB 195 TATGCATGCAACACCCCTGAAGTTCAGTCCATCTTGAAGATCTCCCACTCAGGAGCCT 254
QY 241 GAGCTTATGAATGCAACCCCTCTCTCCACCAAGTCTTCTCAGCAAAATCAACCTTGGC 300
DB 255 GAGCTTATGAATGCAACCCCTCTCTCCACCAAGTCTTCTCAGCAAAATCAACCTTGGC 314
QY 301 CCGTCGTCCCAATCTCATGTCTAAACCATCTGACTTTCACCTTCTTGAAGTGTATCGAAG 360
DB 315 CCGTCGTCCCAATCTCATGTCTAAACCATCTGACTTTCACCTTCTTGAAGTGTATCGAAG 374
QY 361 GGCAGTTTTGGAAGGTTCTTCTAGCAAGACACAGGCGAGAGTGTCTATGCAATC 420
DB 375 GGCAGTTTTGGAAGGTTCTTCTAGCAAGACACAGGCGAGAGTGTCTATGCAATC 434
QY 421 AAAGTTTTTACAGAGAAAGCAATCTCTGAAAGAAAGAGGAGGAGCATATATTATGTCGGAG 480
DB 435 AAAGTTTTTACAGAGAAAGCAATCTCTGAAAGAAAGAGGAGGAGCATATATTATGTCGGAG 494
QY 481 CGGAATGTTCTGTTGAAGATGTGAAGCACCCTTTCTGTTGGGCTTCACTTCTCTTTC 540
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DB 555 CAGACTGCTGACAAATTTGTAATTTGCTCTAGACTACATTAATGTTGAGAGTGTCTTCTAC 614
QY 601 CATCTCAGAGGAAAGCCTGCTCTCGAAGAACCCAGGGCTCGTTTCTATGCTGCTGAAATA 660
DB 615 CATCTCAGAGGAAAGCCTGCTCTCGAAGAACCCAGGGCTCGTTTCTATGCTGCTGAAATA 674
QY 661 GCCAGTGCCTTGGGCTACCTGCATTCATGAACATCGTTTATAGAGACTTAAACACAGAG 720
DB 675 GCCAGTGCCTTGGGCTACCTGCATTCATGAACATCGTTTATAGAGACTTAAACACAGAG 734
QY 721 AATATTTTGTAGATTACAGAGGACACATTTGCTCTTACTGACTCTCGAAGGAG 780
DB 735 AATATTTTGTAGATTACAGAGGACACATTTGCTCTTACTGACTCTCGAAGGAG 794

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QY 781 AACATTGAACACACAGCAGCAACATCCACCTT-CTGTGGCAGCC---GGAGTATCTCGC 836
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QY 837 ACTGAGGTGCTTCATAGCAGCCTT 862
DB 855 CCTGGAGTGCCTTCATAAGCAGCCTT 880

RESULT 2
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LOCUS AGENCOURT 6409166 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5498261
DEFINITION 5', mRNA sequence.
ACCESSION BM455819
VERSION BM455819.1 GI:18504859
SOURCE EST.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1072)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12129 row: 1 column: 06
High quality sequence stop: 640.

FEATURES
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/db_xref="taxon:9606"
/clone="IMAGE:5498261"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: lymph. Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 Kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH MGC Library."
BASE COUNT 282 a 277 c 250 g 262 t 1 others
ORIGIN

Query Match 60.4%; Score 808.4; DB 13; Length 1072;
Best Local Similarity 94.4%; Pred. No. 3.6e-218;
Matches 903; Conservative 0; Mismatches 47; Indels 7; Gaps 6;

QY 116 TGCCTTTTCATGAGCAGAGGAGGATGGGTCTGACGACTTTATTTCAGAGATTGCCAATA 175
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QY 176 ACTCTCTATGCATGCAACACCCCTTCAAGTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG 235
DB 178 ACTCTCTATGCATGCAACACCCCTTCAAGTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG 237
QY 236 AGCTGAGCTTATGAATGCAACCCCTTCTCTCCACCAAGTCTCTTCAGCAAAATCAACC 295
DB 238 AGCTGAGCTTATGAATGCAACCCCTTCTCTCCACCAAGTCTCTTCAGCAAAATCAACC 297
QY 296 TTGGCCCGCTCGTCCCAATCTCATGCTAAACCACTCTGACTTTTCACTTCTTGAAGTGTATCG 355
DB 298 TTGGCCCGCTCGTCCCAATCTCATGCTAAACCACTCTGACTTTTCACTTCTTGAAGTGTATCG 357
QY 356 GAAAGGGCAGTTTTTGGAAAGGTTTCTTCTAGCAAGACACAAAGGAGGAGTGTCTTCTATG 415

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Db 358 GAAAGGCGAGTTTGGAAAGGTTCTTACAGACACAAAGGAGAGAGTGTCTATG 417
Qy 416 CAGTCAAAGTTTACAGAAAGCAATCTCTGAAAGAAAGAGGAGAGCATATATGT 475
Db 418 CAGTCAAAGTTTACAGAAAGCAATCTCTGAAAGAAAGAGGAGAGCATATATGT 477
Qy 476 CGAGCGGAATGTTCTGTTGAAGATGTGAAGACACCTTTCTGTTGGGCTTCACTTCT 535
Db 478 CGAGCGGAATGTTCTGTTGAAGATGTGAAGACACCTTTCTGTTGGGCTTCACTTCT 537
Qy 536 CTTTCCAGACTGCTGACAAATGTGCTTCTCTAGACTACATTAATGTGGAGAGTTGT 595
Db 538 CTTTCCAGACTGCTGACAAATGTGCTTCTCTAGACTACATTAATGTGGAGAGTTGT 597
Qy 596 TCTACCATCTCCAGAGGAAAGCGTCTTCTGAAACCAAGCGGCTCGTTTCTATGCTGCTG 655
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Qy 894 AGCTGCTTGTATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 953
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Qy 954 AATGTAGCAACAACTTCTGAAAGCCTCTCCAGCTGAAACCAAAATATACAAATTCCTG 1013
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Qy 1014 AAGACACTCTGAGGCTCTC - TGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1068
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LOCUS 602970006F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5109625 5',
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ACCESSION BI259163
VERSION BI259163.1 GI:14816226
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 887)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

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/clone="IMAGE:5109625"
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/lab_type="cervical carcinoma cell line"
/lab_host="DH10B"
/Note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: Sali; Cloned unidirectionally. Primer: -Oligo dt.
Average insert size 1.4 kb. Library prepared by Life
Technologies."
BASE COUNT 245 a 214 c 207 g 221 t
ORIGIN
Query Match 59.5%; Score 795.8; DB 13; Length 887;
Best Local Similarity 98.1%; Pred. No. 1.2e-214;
Matches 858; Conservative 0; Mismatches 12; Indels 5; Gaps 5;
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Qy 434 AGAAGCAATCTGAAAAAGAAAGAGAGAGACATATTATGTCGAGCGGAATGTTCTGT 493
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Qy 554 AATTGTACTTGTCTCTAGACTACATTAATGTTGGAGAGTTGTTCTACCACTCTCCAGAGG 613
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Qy 854 AGCAGCTTATGACAGACTGTGAGCTGTGCTGCTGAGAGTGTCTTGTATGAGATGC 913
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Qy 914 TGTATGCTGCTGCGCTTTTATAGCCGAAACACAGCTGAAATGTACGACCAACATTTCTGA 973
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[illegible]

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Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 2 kb. Library constructed by Life
Technologies."

BASE COUNT 235 a 218 c 207 g 227 t 1 others
ORIGIN

Query Match 56.6%; Score 757.2; DB 14; Length 888;
Best Local Similarity 99.6%; Pred. No. 1.1e-203;
Matches 759; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 123 ACTCTATGATGCAACACCCCTGAAGTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG 182
QY 236 AGCTGAGCTTATGAATGCCAACCCCTTCTCTCCACCAAGTCTTTCAGCAAAATCAACC 295
DB 183 AGCTGAGCTTATGAATGCCAACCCCTTCTCTCCACCAAGTCTTTCAGCAAAATCAACC 242
QY 296 TTGGCCCGTCTGCTCAATCCTCATGCTAAACCATCTGACTTTCATCTTGAAGTGTATG 355
DB 243 TTGGCCCGTCTGCTCAATCCTCATGCTAAACCATCTGACTTTCATCTTGAAGTGTATG 302
QY 356 GAAAGGCGAGTTTGGAAAGGTTCTCTAGCAACACCAAGGAGGAGAGAGTGTCTATG 415
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QY 416 CAGTCAAAAGTTTACAGAGAAAGCAATCCTGAAAGAAAGAGGAGAGCAATATATGT 475
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DB 783 CACTGAGTGTCTTATAGCAGGCTTATGACAGGACTGTGG 824

RESULT 6
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DEFINITION AGENCOURT 10056510 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6480313
5', mRNA sequence.
ACCESSION BQ936977
VERSION BQ936977.1 GI:22352360
KEYWORDS EST.

SOURCE
ORGANISM

human.

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 938)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>,

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.llnl.gov>

Plate: LCM2659 row: 0 column: 02

High quality sequence stop: 656.

FEATURES

Location/Qualifiers

1..938

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/clone="IMAGE:6480313"

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/tissue_type="carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/notes="Organ: prostate; Vector: pOTB7; Site: 1: XhoI;

Site: 2: EcoRI; cDNA made by oligo-dT priming. The

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCAGGAG(G). Library constructed by

Ling Hong in the laboratory of Gerald M. Rubin (University

of California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."

BASE COUNT 238 a 255 c 227 g 217 t 1 others

ORIGIN

Query Match 56.2%; Score 751.6; DB 14; Length 938;

Best Local Similarity 98.2%; Pred. No. 4.6e-202;

Matches 803; Conservative 0; Mismatches 9; Indels 6; Gaps 4;

QY 1 ATGGGGAGATGACGGCGCTGGCCAGAGCCCGCTCGAGTCCCTGCTGCGGCCCGCCG 60

DB 60 ATGGGGAGATGACGGCGCTGGCCAGAGCCCGCTCGAGTCCCTGCTGCGGCCCGCCG 119

QY 61 CACAAAAGAGGCCCGAGGCGGAGAAAGAGGAGGAGTCTTCTGCTGAGCGGACTGGCT 120

DB 120 CACAAAAGAGGCCCGAGGCGGAGAAAGAGGAGGAGTCTTCTGCTGAGCGGACTGGCT 179

QY 121 TTTATGAGCAGAGGAGGATGGGTCTGAACGACTTTATTTCAGAGAGATTGCCAATACTCC 180

DB 180 TTTATGAGCAGAGGAGGATGGGTCTGAACGACTTTATTTCAGAGAGATTGCCAATACTCC 239

QY 181 TATGATGCAACACCCCTGAAAGTTAGTCCATCTTGAAGATCTCCCAACCTCAGGAGCCT 240

DB 240 TATGATGCAACACCCCTGAAAGTTAGTCCATCTTGAAGATCTCCCAACCTCAGGAGCCT 299

QY 241 GAGCTTATGATGCCAACCCCTTCTCTCCACCAAGTCTTCTCAGCAAAATCAACCTTGGC 300

DB 300 GAGCTTATGATGCCAACCCCTTCTCTCCACCAAGTCTTCTCAGCAAAATCAACCTTGGC 359

QY 301 CCGTCTGCAATCTCATGCTAAACCATCTGACTTTTCACTTTCTTGAAGATGTCGGAAG 360

DB 360 CCGTCTGCAATCTCATGCTAAACCATCTGACTTTTCACTTTCTTGAAGATGTCGGAAG 419

QY 361 GGCAGTTTTGGAAGGTTCTTCTAGCAAGACACAAGGAGGAGAGTGTCTTATGCAATC 420

DB 420 GGCAGTTTTGGAAGGTTCTTCTAGCAAGACACAAGGAGGAGAGTGTCTTATGCAATC 479

QY 421 AAAGTTTACAGAAAGAAAGCAATCTCTGAAAGAAAGAGGAGAGCAATATATGTCGAG 480

DB 480 AAAGTTTACAGAAAGAAAGCAATCTCTGAAAGAAAGAGGAGAGCAATATATGTCGAG 539

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QY 481 CGGAATGTTCTGTGAGAGATGTGAAGCACCCTTTCTCTGTGGCCCTTCACTTCTCTTTC 540
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Db 540 CGGAATGTTCTGTGAGAGATGTGAAGCACCCTTTCTCTGTGGCCCTTCACTTCTCTTTC 599
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QY 541 CAGACTCTGACAAATGTACTTTGTCTAGACTACATTAATGTTGAGAGTTGTTCTAC 600
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QY 601 CATCTCCAGAGGAAACGCTCTCTCTGGAACACAGGCTCGTTTCTATGCTGCGAAATA 660
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    |||
QY 661 GCCAGTGCCTTGGCTACCTGCACTTCACTGAACATCGTTTATAGAGACTTAAACCA-GA 719
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Db 720 GCCAGTGCCTTGGCTACCTGCACTTCACTGAACATCGTTTATAGAGACTTAAACCA-GA 779
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QY 720 GAATATTTTGTAGATTACACAGG--ACACATTTGCTCTTACTGACTTC-GGACTCTGCAA 776
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Db 780 GAATATTTTGTAGATTACACAGG--ACACATTTGCTCTTACTGACTTCGCACTCTGCAA 839
    |||
QY 777 GGAGAA--CATTTGAACAAACAGCACAAACATCCACCTT 812
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Db 840 GGAGAAACCATTTGAACAAACAGCCCCACATCCCCCTT 877
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RESULT 7
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LOCUS
DEFINITION BQ934765 982 bp mRNA linear EST 21-AUG-2002
AGENCOURT 8837001 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:6429403
5', mRNA sequence.
ACCESSION BQ934765
VERSION BQ934765.1 GI:22350148
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 982)
REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM2617 row: i column: 20
High quality sequence stop: 683.
Location/Qualifiers
1..982
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6429403"
/clone_lib="NIH_MGC_101"
/tissue_types="epidermoid carcinoma, cell line"
/lab_hosts="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
254 a 251 c 240 g 236 t 1 others
BASE COUNT
ORIGIN
Query Match 55.8%; Score 746.4; DB 14; Length 982;

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Best Local Similarity 98.5%; Pred. No. 1.4e-200;
Matches 806; Conservative 0; Mismatches 6; Indels 6; Gaps 5;

QY 1 ATGGGGGAGATGAGGGCGCGCTGGCCAGAGCCGGCTCGAGTCCCTGCTGCGGGCCCCGC 60
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Db 14 ATGGGGGAGATGAGGGCGCGCTGGCCAGAGCCGGCTCGAGTCCCTGCTGCGGGCCCCGC 73
    |||
QY 61 CACAAAGAGGGCGGAGGGCGGAGAAAGAGGAGTCTTCTCTGCTGAGCGGACTGGCT 120
    |||
Db 74 CACAAAGAGGGCGGAGGGCGGAGAAAGAGGAGTCTTCTCTGCTGAGCGGACTGGCT 133
    |||
QY 121 TTTCATGAGCAGAGGAGGATGGTCTGAAACGACTTTATTTCAGAAAGATTGCGCAATAACTCC 180
    |||
Db 134 TTTCATGAGCAGAGGAGGATGGTCTGAAACGACTTTATTTCAGAAAGATTGCGCAATAACTCC 193
    |||
QY 181 TATGATGCAACACCCCTGAAAGTTTCACTTCTGAAAGATCTCCCACTCAGGAGCCT 240
    |||
Db 194 TATGATGCAACACCCCTGAAAGTTTCACTTCTGAAAGATCTCCCACTCAGGAGCCT 253
    |||
QY 241 GAGCTTATGATGCAACCCCTTCTCTCCAGCAAGTCTTCTCAGCAAAATCAACCTTGGC 300
    |||
Db 254 GAGCTTATGATGCAACCCCTTCTCTCCAGCAAGTCTTCTCAGCAAAATCAACCTTGGC 313
    |||
QY 301 CGCTCGTCCAATCCTCATGCTAAACCATCTGACTTTTCACTTCTTGAAGTGTATCGGAAG 360
    |||
Db 314 CGCTCGTCCAATCCTCATGCTAAACCATCTGACTTTTCACTTCTTGAAGTGTATCGGAAG 373
    |||
QY 361 GGAGTGTGGAAGGTTCTTTAGCAAGACACAGGAGAGAAAGTGTCTATGAGTGC 420
    |||
Db 374 GGAGTGTGGAAGGTTCTTTAGCAAGACACAGGAGAGAAAGTGTCTATGAGTGC 433
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QY 421 AAGTGTTCAGAGAAAGCAATCTCTGAAAGAGAGAGAGAGATATATATGTCGGAG 480
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Db 434 AAGTGTTCAGAGAAAGCAATCTCTGAAAGAGAGAGAGATATATATGTCGGAG 493
    |||
QY 481 CGGAATGTTCTGTGTAAGAAATGTGAAGCACCCTTTCTCTGTGGCCCTTCACTTCTCTTTC 540
    |||
Db 494 CGGAATGTTCTGTGTAAGAAATGTGAAGCACCCTTTCTCTGTGGCCCTTCACTTCTCTTTC 553
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QY 541 CAGACTGCTGACAAATGTACTTTGTCTAGACTACATTAATGCTGAGAGTTGTTCTAC 600
    |||
Db 554 CAGACTGCTGACAAATGTACTTTGTCTAGACTACATTAATGCTGAGAGTTGTTCTAC 613
    |||
QY 601 CATCTCCAGAGGAAACGCTCTCTGGAACACAGGCTCGTTTCTATGCTGCGAAATA 660
    |||
Db 614 CATCTCCAGAGGAAACGCTCTCTGGAACACAGGCTCGTTTCTATGCTGCGAAATA 673
    |||
QY 661 GCCAGTGCCTTGGCTACCTGCACTTCACTGAACATCGTTTATAGAGACTTAAACCCAGAG 720
    |||
Db 674 GCCAGTGCCTTGGCTACCTGCACTTCACTGAACATCGTTTATAGAGACTTAAACCCAGAG 733
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QY 721 AATATTTGCTAGATTACAGGG-ACACATTTGT-CTTACTGAC-TTCGGACTCT-GCAA 776
    |||
Db 734 AATATTTGCTAGATTACAGGGNACATATGTCCTTACTGACTTTTCGGACTCTGCGAG 793
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QY 777 GGAGACATTTGAACAA--CAGCACAAATCCACCTT 812
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Db 794 GGAGACATTTGAACAA--CAGCACAAATCCACCTT 831
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RESULT 8
LOCUS
DEFINITION BQ934765 851 bp mRNA linear EST 25-SEP-2001
603051130F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5191422 5',
mRNA sequence.
ACCESSION BQ934765
VERSION BQ934765.1 GI:15756574
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 851)
REFERENCE

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AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-x@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
 Plate: LAM11478 row: k column: 07
 High quality sequence start: 3
 High quality sequence stop: 756.

FEATURES

Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5191422"
 /lab_host="DH10B"
 /note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH MGC Library."
 215 a 225 c 199 g 212 t

BASE COUNT
ORIGIN

Query Match 54.6%; Score 730.2; DB 13; Length 851;
 Best Local Similarity 99.5%; Pred. No. 5.2e-196;
 Matches 743; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 592 TTGTTCTACCATCTCCAGAGGAACTGCTTCTCGAAGCAGCGGCTCGTTCTATGCT 651
 1 TTGTTCTACCATCTCCAGAGGAACTGCTTCTCGAAGCAGCGGCTCGTTCTATGCG 60
 652 GCTGAATAGCCAGTGTCTGGGCTACTGCAATTCATGAACATCGTTTATAGACTTA 711
 61 GCTGAATAGCCAGTGTCTGGGCTACTGCAATTCATGAACATCGTTTATAGACTTA 120
 712 AAACGAGAAATATTTGCTAGATTACAGGACACATGTCCTTACTGACTTCGGACTC 771
 121 AAACGAGAAATATTTAGTAGATTACAGGACACATGTCCTTACTGACTTCGGACTC 180
 772 TGCAGGAGACATTGAACACACAGACACATCCACCTCTGTGCGACGCGGAGTAT 831
 181 TGCAGGAGACATTGAACACACAGACACATCCACCTCTGTGCGACGCGGAGTAT 240
 832 CTGCACTCAGGTGCTTCTAAGCAGCTTATGACAGGACTGTGGACTGGTGTGCTG 891
 241 CTGCACTCAGGTGCTTCTAAGCAGCTTATGACAGGACTGTGGACTGGTGTGCTG 300
 892 GGAGCTGCTTGTATGAGATGCTGTATGGCTGCGGCTTTTATAGCCGAAACACAGCT 951
 301 GGAGCTGCTTGTATGAGATGCTGTATGGCTGCGGCTTTTATAGCCGAAACACAGCT 360
 952 GAATGTGACACACATCTGAACAGCTTCTGAGTGAACCAATATACAAATTC 1011
 361 GAATGTGACACACATCTGAACAGCTTCTGAGTGAACCAATATACAAATTC 420
 1012 GCAAGACACCTCTCGAGGCGCTCTCGAGAGGACAGGACAAAGCGGCTCGGGCCAG 1071
 421 GCAAGACACCTCTCGAGGCGCTCTCGAGAGGACAGGACAAAGCGGCTCGGGCCAG 480
 1072 GATGACTTCATGGAGATTAAAGATCATGTCTTCTCTTAATTAACCTGGGATGATCTC 1131

Db 481 GATGACTTCATGGAGATTAAAGATCATGTCTTCTCTTAATTAACCTGGGATGATCTC 540
 QY 1132 ATTAATAAGAAGATTACTCCCTTTTAAACCCAAATGTGAGTGGGCCCAACGACCTACGG 1191
 Db 541 ATTAATAAGAAGATTACTCCCTTTTAAACCCAAATGTGAGTGGGCCCAACGACCTACGG 600
 QY 1192 CACTTTGACCCGAGTTTACCGAAGAGCTGTGCCCAACTCCATTGGCAAGTCCCTGAC 1351
 Db 601 CACTTTGACCCGAGTTTACCGAAGAGCTGTGCCCAACTCCATTGGCAAGTCCCTGAC 660
 QY 1252 AGCGTCTCGTCACAGCCGAGCTCAAGAGAGCTGCGGAGCTTCTTAGGCTTTCTCTAT 1311
 Db 661 AGCGTCTCGTCACAG-CAGCGTCAAGAGAGCTGCGGAGCTTCTTAGGCTTTCTCTAT 719
 QY 1312 GCGCTCTCCACGAGCTCTTCTCTCTGA 1338
 Db 720 GCGCTCTCCACGAGCTCTTCTCTCTGA 746
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 AUI134278
 LOCUS AUI134278 741 bp mRNA linear EST 01-AUG-2002
 DEFINITION AUI134278 OVARC1 Homo sapiens cDNA clone OVARC1001642 5', mRNA sequence.
 ACCESSION AUI134278
 VERSION AUI134278.1 GI:10994817
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 741)
 REFERENCE Ota.T., Nishikawa.T., Suzuki.Y., Ishii.S., Saito.K., Kawai.Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.
 TITLE HRI human cDNA project
 JOURNAL Unpublished (2000)
 COMMENT Contact: Takao Isogai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
 Location/Qualifiers
 1..741
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 /tissue_type="ovary, tumor tissue"
 /note="Vector: pME18SFL3"
 BASE COUNT 209 a 168 c 179 g 182 t 3 others
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 Query Match 53.3%; Score 712.8; DB 9; Length 741;
 Best Local Similarity 99.1%; Pred. No. 4.2e-191;
 Matches 736; Conservative 0; Mismatches 5; Indels 2; Gaps 2;
 QY 343 TTGAAGTATCGGAAGGCGAGTTTGGAAAGGTTCTTCTAGCAGACACAGGCGAA 402
 Db 1 TTGAAGTATCGGAAGGCGAGTTTGGAAAGGTTCTTCTAGCAGACACAGGCGAA 60
 QY 403 GAAGTGTCTTATGCACTCAAAAGTTTTCAGAGAAAGCAATCTGAAAAAGAGGAG 462
 Db 61 GAAGTGTCTTATGCACTCAAAAGTTTTCAGAGAAAGCAATCTGAAAAAGAGGAG 120
 QY 463 AAGCATATTATGTGCGGCGGAATGTTCTGTTGAAGAATGTGAAGCACCCCTTTCTGCTG 522

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121 AAGCATATTATGTCGGAGCGGAATGTTCTGTGGAAGATGGAAGCACCTTCTCTGTTG 180
122 AAGCATATTATGTCGGAGCGGAATGTTCTGTGGAAGATGGAAGCACCTTCTCTGTTG 180
523 GGCCTTCACTTCTCTTTCAGAGCTGCTGACAAATGTAATGTAATGTAATGTAATGTAAT 582
181 GGCCTTCACTTCTCTTTCAGAGCTGCTGACAAATGTAATGTAATGTAATGTAATGTAAT 240
583 GGTGGAGAGTTGTTCTACCACTCTCCAGAGGAGCGCTGCTTCTCTGGAACCAACGGCTCGT 642
241 GGTGGAGAGTTGTTCTACCACTCTCCAGAGGAGCGCTGCTTCTCTGGAACCAACGGCTCGT 300
643 TTCTATGCTGCTGAAATAGGAGGAGCTGCTTCTGAGGAGCTGCTGCTGCTGCTGCTGCT 702
301 TTCTATGCTGCTGAAATAGGAGGAGCTGCTTCTGAGGAGCTGCTGCTGCTGCTGCTGCT 360
703 AGAGACTTAAACCAAGAGAGATATTTTCTGATGATGATGATGATGATGATGATGATGAT 762
361 AGAGACTTAAACCAAGAGAGATATTTTCTGATGATGATGATGATGATGATGATGATGAT 420
763 TTGGAGCTCTGCAAGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 822
421 TTGGAGCTCTGCAAGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
823 CCGAGGATCTCGCACCTGAGGAGCTTCTGATGATGATGATGATGATGATGATGATGATG 882
481 CCGAGGATCTCGCACCTGAGGAGCTTCTGATGATGATGATGATGATGATGATGATGATG 540
883 TGTGCTCTGGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 942
541 TGTGCTCTGGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
943 AACACAGCTGAAATGTAAGCAACATTTCTGAAAGAGCTTCTGAAAGAGCTTCTGAAAG 1002
601 AACACAGCTGAAATGTAAGCAACATTTCTGAAAGAGCTTCTGAAAGAGCTTCTGAAAG 660
1003 ACAAATCCGCAAGACACCTCTGAGGAGGCTCTGAGAGGAGGAGGAGGAGGAGGAGGAG 1062
661 ACAAATCCGCAAGACACCTCTGAGGAGGCTCTGAGAGGAGGAGGAGGAGGAGGAGGAG 718
1063 GGGGCCAAGAGTACCTCATGGA 1085
719 GGGGCCAAGAGTACCTCATGGA 741

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RESULT 10
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DEFINITION 602597986F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4706829 5',
mRNA sequence.
ACCESSION BG575325
VERSION BG575325.1 GI:13582978
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 736)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10575 row: k column: 22
High quality sequence stop: 732.
Location/Qualifiers
1. 736

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FEATURES

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/lab_host="DH10B (phage-resistant)"
/notes="Organ: breast; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH MGC Library."
BASE COUNT 186 a 205 c 168 g 177 t
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Best Local Similarity 98.8%; Pred. No. 3e-190;
Matches 726; Conservative 0; Mismatches 7; Indels 2; Gaps 1;
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DB 1 CTCAGAGGGAACGCTGCTTCTCTGGAACCAACGGGCTCGTTTCTATGCTGCTGAAATAGCC 60
QY 664 AGTGCCTTGGGCTACCTGCAATTCACCTGAAATGTAAGAGACTTAAACACAGAGAAT 723
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DB 121 ATTTTCTAGATTCACAGGAGACATTTGCTTCTTCTGACTTCTGCAAGGAGAAC 180
QY 784 ATTGAACACAAAGAGCTCTCCAGCTGAAACCAAAATATTACAAATTTCCGCAAGACACCTC 843
DB 181 ATTGAACACAAAGAGCTCTCCAGCTGAAACCAAAATATTACAAATTTCCGCAAGACACCTC 240
QY 844 GTGCTTTATAAGCAGCCTTATGACAGGACTGTGGAGCTGTGGTGTGCTGGAGAGTGTCTTG 903
DB 241 GTGCTTTATAAGCAGCCTTATGACAGGACTGTGGAGCTGTGGTGTGCTGGAGAGTGTCTTG 300
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QY 964 AACATTCTGAACAAAGCTCTCCAGCTGAAACCAAAATATTACAAATTTCCGCAAGACACCTC 1023
DB 361 AACATTCTGAACAAAGCTCTCCAGCTGAAACCAAAATATTACAAATTTCCGCAAGACACCTC 420
QY 1024 CTGAGAGGCTCTCTGAGAGGAGACAGGACAAAGCGCTCGGGCCCAAGGATGACTTCATG 1083
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DB 481 GAGATTAAAGAGTATGCTTCTTCTCTTAAATTAACCTGGAGTATCTCATTAATAAGAAG 540
QY 1144 ATTACTCCCCCTTTTAAACCAAAATGAGTGGGCCCAACAGACCTAGCGCACTTTGACCCC 1203
DB 541 ATTACTCCCCCTTTTAAACCAAAATGAGTGGGCCCAACAGACCTAGCGCACTTTGACCCC 600
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DB 601 GAGTTTACCGAAGAGCCTGTCCCAACTCCATTTGGCAAGTCCCTGACAGCTCTCGTGC 660
QY 1264 ACAGCCAGGCTCAAGAGCTGCGGAGGCTTCTTAGGCTTTTCTTAGGCTTTTCTTAGGCT 1323
DB 661 ACAGC-AGCGTCAGGAAGCTGCGGAGGCTTCTTAGGCTTTTCTTAGGCTTTTCTTAGGCT 718
QY 1324 GACTCTTCTCTGTA 1338
DB 719 GACTCTTCTCTGTA 733

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RESULT 11
ALS30006

LOCUS AL530006 811 bp mRNA linear EST 13-FEB-2001
 DEFINITION AL530006 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DD009YH16 5
 prime, mRNA sequence.
 ACCESSION AL530006
 VERSION AL530006.1 GI:12793499
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 811)
 AUTHORS Li W.B., Gruber C., Jesse J., and Polayes D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source

1..811
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="CS0DD009YH16"
 /clone_lib="LTI_NFL001_NBC4"
 /sex="male"
 /tissue_type="neuroblastoma cells"
 /lab_host="DH10B"
 /notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed
 by Life Technologies. Contact : Feng Liang Life
 Technologies, a division of Invitrogen 9800 Medical Center
 Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
 8371 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT 221 a 200 c 180 g 210 t
 ORIGIN

Query Match 52.9%; Score 707.4; DB 9; Length 811;
 Best Local Similarity 99.9%; Pred. No. 1.5e-189;
 Matches 708; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 116 TGGCTTTTCATGAAGCAGAGGAGGATGGTCTGAACGACTTTATTCAGAAGATTGCCAATA 175
 DB 103 TCGCTTTTCATGAAGCAGAGGAGGATGGTCTGAACGACTTTATTCAGAAGATTGCCAATA 162
 QY 176 ACTCCTATGATGCAAAACACCTGAAGTTGAGTCCATCTTGAAGATCTCCAACTCAGG 235
 DB 163 ACTCCTATGATGCAAAACACCTGAAGTTGAGTCCATCTTGAAGATCTCCAACTCAGG 222
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RESULT 12

BI333256

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

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/lab_host="DH10B"

/notes="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.4 kb. Library prepared by Life
 Technologies."

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ORIGIN

Query Match

Best Local Similarity

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0; Indels

0; Gaps

0;
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VERSION
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    NIH-MGC http://mgc.nci.nih.gov/.
    National Institutes of Health, Mammalian Gene Collection (MGC)
    Unpublished (1999)
    Contact: Robert Strausberg, Ph.D.
    Email: cgapbs-r@mail.nih.gov
    Tissue Procurement: ATCC
    cDNA Library Preparation: Life Technologies, Inc.
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    DNA Sequencing by: Agencourt Bioscience Corporation
    Clone distribution: MGC clone distribution information can be
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    http://image.llnl.gov
    Plate: LLAM12214 row: 0 column: 24
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 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
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 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library." |"
 BASE COUNT 221 a 210 c 196 g 217 t 1 others
 ORIGIN

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Best Local Similarity 97.4%; Pred. No. 5.7e-187;

Matches 742; Conservative 0; Mismatches 16; Indels 4; Gaps 3;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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10	410.4	30.7	423	10	US-09-925-300-860
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12	351.6	26.3	851	9	US-09-764-868-56
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14	263.4	19.7	404	10	US-09-960-352-7426
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ALIGNMENTS

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; GENERAL INFORMANT:
; APPLICANT: Au-Young, Janice
; Guegler, Karl J.
; Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/810,808
; FILING DATE: 15-Mar-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/541,228
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0118 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2311 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

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; IMMEDIATE SOURCE:
; LIBRARY: <Unknown>
; CLONE: Consensus
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-810-808-6

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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1221; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 803 CACTGAGGTGCTTTCATAGCAGCCTTATGACAGGACTGTGGACTGTGTGCTGGGAG 862
QY 896 CTGTCTTGTATGAGATGCTGTATGGCTGCGGCTTTTATAGCCGAAACACAGCTGAAA 955
DB 863 CTGTCTTGTATGAGATGCTGTATGGCTGCGGCTTTTATAGCCGAAACACAGCTGAAA 922
QY 956 TGTACGACAAACATTCTGAAACAGGCTCTCCAGCTGAAACCAAAATATTACAAATTCGCA 1015
DB 923 TGTACGACAAACATTCTGAAACAGGCTCTCCAGCTGAAACCAAAATATTACAAATTCGCA 982
QY 1016 GACACTCTCGAGGGCTCTCTCGAGAGAGACAGGACAAAGCGGCTCGGGGCCAAGATG 1075
DB 983 GACACTCTCGAGGGCTCTCTCGAGAGAGACAGGACAAAGCGGCTCGGGGCCAAGATG 1042

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RESULT 2
US-09-981-353-6
; Sequence 6, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Laeek, Amy W.
; APPLICANT: Jones, David A.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 2365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 3819039CB1
US-09-981-353-6

Query Match      91.2%; Score 1219.8; DB 9; Length 2365;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1221; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 116 TGGCTTTCATGAAGCAGAGAGAGATGGTCTGAACGACTTTATTCAGAAAGATTGCCAATA 175
DB 134 TGGCTTTCATGAAGCAGAGAGAGATGGTCTGAACGACTTTATTCAGAAAGATTGCCAATA 193
QY 176 ACTCCTATGATGCAAAACACCCCTGAAGTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG 235
DB 194 ACTCCTATGATGCAAAACACCCCTGAAGTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG 253
QY 236 AGCTGAGCTTATGAATGCCAACCCCTTCTCTCCACCAAGTCTCTTCAGCAAAATCAACC 295
DB 254 AGCTGAGCTTATGAATGCCAACCCCTTCTCTCCACCAAGTCTCTTCAGCAAAATCAACC 313
QY 296 TTGGCCCGTCCGTCCTCATGCTAAACCATCTGACTTTTCACTTTCTTGAAGTGTATG 355
DB 314 TTGGCCCGTCCGTCCTCATGCTAAACCATCTGACTTTTCACTTTCTTGAAGTGTATG 373
QY 356 GAAAGGCGAGTTTGGAAAGGTTCTTCTAGCAAGACACAAGGAGAGAGTGTCTATG 415
DB 374 GAAAGGCGAGTTTGGAAAGGTTCTTCTAGCAAGACACAAGGAGAGAGTGTCTATG 433
QY 416 CAGTCAAAAGTTTACAGAAAGAGCAATCTGAAAGAAAGAGAGAGCAATATATGT 475
DB 434 CAGTCAAAAGTTTACAGAAAGAGCAATCTGAAAGAAAGAGAGAGCAATATATGT 493
QY 476 CGGAGCGGAATGTTCTGTTGAAGAAATGTGAAGACCCCTTTCTGTTGGTGGCTTCACTTCT 535

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Db 494 CGGAGCGAATGTTCTGTTGAAGAATGTGAAGCACCCCTTCTCGTGGGCGCTTCACTTCT 553
Qy 536 CTTTCCAGACTGCTGACAAATTTGACTTTCTGCTAGACTACATTAATGGTGGAGAGTTGT 595
Db 554 CTTTCCAGACTGCTGACAAATTTGACTTTCTGCTAGACTACATTAATGGTGGAGAGTTGT 613
Qy 596 TCTACCATCTCCAGAGGAAACGCTGCTTCTGGAACACACGGGCTGCTTCTATGCTGCTG 655
Db 614 TCTACCATCTCCAGAGGAAACGCTGCTTCTGGAACACACGGGCTGCTTCTATGCTGCTG 673
Qy 656 AAATAGCCAGTCTTGGGCTACTGCTGCTTCTGGAACACACGGGCTGCTTCTATGCTGCTG 715
Db 674 AAATAGCCAGTCTTGGGCTACTGCTGCTTCTGGAACACACGGGCTGCTTCTATGCTGCTG 733
Qy 716 CAGAGAATATTTGCTAGATTTCAGGGACACATTTGCTTACTGACTTCGGACTCTGCA 775
Db 734 CAGAGAATATTTGCTAGATTTCAGGGACACATTTGCTTACTGACTTCGGACTCTGCA 793
Qy 776 AGGAGAAATGTAACACAAACAGCACACATCCACCTTCTGTCGACGCCGGAGTATCTCG 835
Db 794 AGGAGAAATGTAACACAAACAGCACACATCCACCTTCTGTCGACGCCGGAGTATCTCG 853
Qy 836 CACTGAGTGCTTCATAAGCAGCTTATCAGAGGACTGTCGACTGCTGCTGGGAG 895
Db 854 CACTGAGTGCTTCATAAGCAGCTTATCAGAGGACTGTCGACTGCTGCTGGGAG 913
Qy 896 CTGCTTGTATGAGTCTGTATGGCTGCGGCTTTTATAGCCGAAACACAGCTGAAA 955
Db 914 CTGCTTGTATGAGTCTGTATGGCTGCGGCTTTTATAGCCGAAACACAGCTGAAA 973
Qy 956 TGACGAAATATTTGAAACAGCTCTCCAGCTGAAACCAATATTTACAAATTCGCGAA 1015
Db 974 TGACGAAATATTTGAAACAGCTCTCCAGCTGAAACCAATATTTACAAATTCGCGAA 1033
Qy 1016 GACACTCTCGAGGGCTCTCTGAGAGGACGAGGACAAAGCGCTCGGGGCCAAGGATG 1075
Db 1034 GACACTCTCGAGGGCTCTCTGAGAGGACGAGGACAAAGCGCTCGGGGCCAAGGATG 1093
Qy 1076 ACTTCATGAGATTAAGAGTCATGCTTCTTCTCTTAAATTAAGTGGATGATCTCATTA 1135
Db 1094 ACTTCATGAGATTAAGAGTCATGCTTCTTCTCTTAAATTAAGTGGATGATCTCATTA 1153
Qy 1136 ATAAGAAGATTACTCCCTCTTTAAACCAATGTGAGTGGGCCCAACGACTACGGCACT 1195
Db 1154 ATAAGAAGATTACTCCCTCTTTAAACCAATGTGAGTGGGCCCAACGACTACGGCACT 1213
Qy 1196 TTGACCCGAGTTTACCGAAGAGCTGTCCCAACTCCATTTGGCAAGTCCCTTGACAGCG 1255
Db 1214 TTGACCCGAGTTTACCGAAGAGCTGTCCCAACTCCATTTGGCAAGTCCCTTGACAGCG 1273
Qy 1256 TCCTCGTCAGCAGCGGTCAAGAGCTGCCGAGGCTTCTTAGGCTTTTCTATGCGC 1315
Db 1274 TCCTCGTCAGCAGCGGTCAAGAGCTGCCGAGGCTTCTTAGGCTTTTCTATGCGC 1333
Qy 1316 CTCCACGGACTCTTCTCTCTGA 1338
Db 1334 CTCCACGGACTCTTCTCTCTGA 1356
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RESULT 3

US-10-000-039-1

; Sequence 1, Application US/10000039

; Publication No. US20030003559A1

; GENERAL INFORMATION:

; APPLICANT: LANG, Florian

; TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY & LARDNER

; STREET: 3000 K Street, N.W.

; CITY: Washington

```
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/000,039
FILING DATE: 04-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/031,295
FILING DATE: 26-FEB-1998
APPLICATION NUMBER: DE 197-08-173.8
FILING DATE: 28-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sanderscock, Collin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 058315/0123
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2370 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 43..1335
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-000-039-1
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Query Match 91.0%; Score 1218.2; DB 9; Length 2370;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 116 TGGCTTTTATGAAGCAGAGGAGGATGGGTCTGAACGACTTTTATTCAGAGATTGCCAATA 175
Db 116 TGGCTTTTATGAAGCAGAGGAGGATGGGTCTGAACGACTTTTATTCAGAGATTGCCAATA 175
Qy 176 ACTCCTATGCATGCAACACCCCTGAAAGTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG 235
Db 176 ACTCCTATGCATGCAACACCCCTGAAAGTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG 235
Qy 236 AGCCTGAGCTTATGAATGCCAACCCCTTCTCCTCCCAAGTCTCTTCAGCAATCAACC 295
Db 236 AGCCTGAGCTTATGAATGCCAACCCCTTCTCCTCCCAAGTCTCTTCAGCAATCAACC 295
Qy 296 TTGGCCCGTCTGTCATCTCTATGTAACCATCTGACCTTTTCACTTTTGAAGTGTATCG 355
Db 296 TTGGCCCGTCTGTCATCTCTATGTAACCATCTGACCTTTTCACTTTTGAAGTGTATCG 355
Qy 356 GAAAGGCGAGTTTGGAGAGGTTCTTCTAGCAGACACAAAGGAGAGGAGTGTCTCTATG 415
Db 356 GAAAGGCGAGTTTGGAGAGGTTCTTCTAGCAGACACAAAGGAGAGGAGTGTCTCTATG 415
Qy 416 CAGTCAAAAGTTTTACAGAAAGAAAGCAATCCTGAAAGAAAGAGGAGAGCATATTATGT 475
Db 416 CAGTCAAAAGTTTTACAGAAAGAAAGCAATCCTGAAAGAAAGAGGAGAGCATATTATGT 475
Qy 476 CGGAGCGGAATGTTCTGTTGAAAGATGTGAAGCACCCCTTCTGTTGGGCGCTTCACTTCT 535
Db 476 CGGAGCGGAATGTTCTGTTGAAAGATGTGAAGCACCCCTTCTGTTGGGCGCTTCACTTCT 535
Qy 536 CTTTCCAGACTGCTGCAAAATTTGTACTTTTGTCTAGACTACATTATATGTTGGAGAGTTGT 595
Db 536 CTTTCCAGACTGCTGCAAAATTTGTACTTTTGTCTAGACTACATTATATGTTGGAGAGTTGT 595
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Qy 596 TCTACCATCTCCAGAGGAAACGCTCTTCTGGAACACACGGGCTCGTTTCTATGCTGCTG 655
Db 596 TCTACCATCTCCAGAGGAAACGCTCTTCTGGAACACACGGGCTCGTTTCTATGCTGCTG 655
Qy 656 AATATAGCAGTGGCTTGGCTGACTGCTGCAATCACTGAAACATCGTTTATAGAGACTTAAAC 715
Db 656 AATATAGCAGTGGCTTGGCTGACTGCTGCAATCACTGAAACATCGTTTATAGAGACTTAAAC 715
Qy 716 CAGAGAAATATTTGCTAGATCTACAGGACACATTTGCTTACTGACTTCGGACTCTGCA 775
Db 716 CAGAGAAATATTTGCTAGATCTACAGGACACATTTGCTTACTGACTTCGGACTCTGCA 775
Qy 776 AGGAGAAATATTTGCTAGATCTACAGGACACATTTGCTTACTGACTTCGGACTCTGCA 835
Db 776 AGGAGAAATATTTGCTAGATCTACAGGACACATTTGCTTACTGACTTCGGACTCTGCA 835
Qy 836 CAGCTGAGTGGCTTCTGAAACAGACATCTCCAGCTGAAACCAATATTTACAAATTTCCGCA 1015
Db 836 CAGCTGAGTGGCTTCTGAAACAGACATCTCCAGCTGAAACCAATATTTACAAATTTCCGCA 1015
Qy 1016 GACACCTCTCGAGGCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1075
Db 1016 GACACCTCTCGAGGCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1075
Qy 1076 ACTTCATGAGATTAAGAGTATGCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1135
Db 1076 ACTTCATGAGATTAAGAGTATGCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1135
Qy 1136 ATAAGAAATATTTACTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1195
Db 1136 ATAAGAAATATTTACTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1195
Qy 1196 TTGACCCGAGTTTACCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1255
Db 1196 TTGACCCGAGTTTACCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1255
Qy 1256 TCCTGTCAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1315
Db 1256 TCCTGTCAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1315
Qy 1316 CTCCACGAGCTCTTCTCTCTGA 1338
Db 1316 CTCCACGAGCTCTTCTCTCTGA 1338

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RESULT 4
US-09-969-347-214
; Sequence 214, Application US/09969347
; Patent No. US20020115085A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-69
; CURRENT APPLICATION NUMBER: US/09/969,347
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,598
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,604
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 318
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 214
; LENGTH: 2370
; TYPE: DNA

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; ORGANISM: Homo sapiens
US-09-969-347-214
Query Match 91.0%; Score 1218.2; DB 10; Length 2370;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 116 TGGCTTTTCAATGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 175
Db 116 TGGCTTTTCAATGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 175
Qy 176 ACTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 235
Db 176 ACTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 235
Qy 236 AGCTGAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 295
Db 236 AGCTGAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 295
Qy 296 TTGGCCCGCTGCTCCCAATCTGCTAAACCATCTGACTTTTCACTTTTCTTTGAAAGTGTATG 355
Db 296 TTGGCCCGCTGCTCCCAATCTGCTAAACCATCTGACTTTTCACTTTTCTTTGAAAGTGTATG 355
Qy 356 GAAAGGCGAGTTTGGAAAGGTTTCTTAGCAAGACACAAGGCGAGAGAGAGAGAGAGATGTTCTATG 415
Db 356 GAAAGGCGAGTTTGGAAAGGTTTCTTAGCAAGACACAAGGCGAGAGAGAGAGAGATGTTCTATG 415
Qy 416 CAGTCAAGTTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGTTATG 475
Db 416 CAGTCAAGTTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGTTATG 475
Qy 476 CGAGCGGAGTGTCTGTTGAAAGATGTAAGCAGCCTTTTCTGTTGGGCTTCTACTTCT 535
Db 476 CGAGCGGAGTGTCTGTTGAAAGATGTAAGCAGCCTTTTCTGTTGGGCTTCTACTTCT 535
Qy 536 CTTTCCAGAGTGTCTGCAAAATTTGACTTTTCTAGACTTACATTAATGTTGGAGAGTGT 595
Db 536 CTTTCCAGAGTGTCTGCAAAATTTGACTTTTCTAGACTTACATTAATGTTGGAGAGTGT 595
Qy 596 TCTACCATCTCCAGAGGAAACGCTCTTCTGGAACACACGGGCTCGTTTCTATGCTGCTG 655
Db 596 TCTACCATCTCCAGAGGAAACGCTCTTCTGGAACACACGGGCTCGTTTCTATGCTGCTG 655
Qy 656 AATATAGCAGTGGCTTGGCTTCTCTGAAACATCTGTTTATAGAGACTTAAAC 715
Db 656 AATATAGCAGTGGCTTGGCTTCTCTGAAACATCTGTTTATAGAGACTTAAAC 715
Qy 716 CAGAGAAATATTTGCTAGATTTACAGGAGACATTTGCTTACTGACTTCGGACTCTGCA 775
Db 716 CAGAGAAATATTTGCTAGATTTACAGGAGACATTTGCTTACTGACTTCGGACTCTGCA 775
Qy 776 AGGAGAAATATTTGCTAGATTTACAGGAGACATTTGCTTACTGACTTCGGACTCTGCA 835
Db 776 AGGAGAAATATTTGCTAGATTTACAGGAGACATTTGCTTACTGACTTCGGACTCTGCA 835
Qy 836 CAGCTGAGTGGCTTCTGAAACAGACATCTCCAGCTGAAACCAATATTTACAAATTTCCGCA 895
Db 836 CAGCTGAGTGGCTTCTGAAACAGACATCTCCAGCTGAAACCAATATTTACAAATTTCCGCA 895
Qy 896 CTGCTTGTATGAGATGCTGTTATGAGGCTTCTGCGCTTTTATAGCCGAAACACAGCTGAAA 955
Db 896 CTGCTTGTATGAGATGCTGTTATGAGGCTTCTGCGCTTTTATAGCCGAAACACAGCTGAAA 955
Qy 956 TGTACGACAAATTTCTGAAACAGACATCTCCAGCTGAAACCAATATTTACAAATTTCCGCA 1015
Db 956 TGTACGACAAATTTCTGAAACAGACATCTCCAGCTGAAACCAATATTTACAAATTTCCGCA 1015
Qy 1016 GACACCTCTCGAGGCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1075
Db 1016 GACACCTCTCGAGGCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1075
Qy 1076 ACTTCATGAGATTAAGAGTATGCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1135
Db 1076 ACTTCATGAGATTAAGAGTATGCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1135

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Db 1076 ACTTCATGGAGATTAAGAGTCATGCTCTTCTCTCTTAATTAACCTGGAGTATCTCATTA 1135
Qy 1136 ATAAGAGATTAATCCCTTTTAAACCAAAATGTGAGTGGGCCCAACGACCTACGGCACT 1195
Db 1136 ATAAGAGATTAATCCCTTTTAAACCAAAATGTGAGTGGGCCCAACGAGCTACGGCACT 1195
Qy 1196 TTGACCCGAGTTTACCGAAGAGCTGTCCCAACTCATTTGGCAAGTCCCTGACAGCG 1255
Db 1196 TTGACCCGAGTTTACCGAAGAGCTGTCCCAACTCATTTGGCAAGTCCCTGACAGCG 1255
Qy 1256 TCCTCGTCACAGCCAGCGTCAAGGAAGCTGCCGAGGCTTTCTTAGGCTTTTCTATGCGC 1315
Db 1256 TCCTCGTCACAGCCAGCGTCAAGGAAGCTGCCGAGGCTTTCTTAGGCTTTTCTATGCGC 1315
Qy 1316 CTCCACGGACTCTTTCTCTGA 1338
Db 1316 CTCCACGGACTCTTTCTCTGA 1338

RESULT 5

US-09-880-107-3855
; Sequence 3855, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3855
; LENGTH: 2370
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 Y10032
US-09-880-107-3855

Query Match 91.08; Score 1218.2; DB 10; Length 2370;
Best Local Similarity 99.88; Pred. No. 0;
Matches 1220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 116 TGGCTTTTCATGAAGCAGAGGAGGATGGTCTGAACGACTTTATTTCAGAAGATTGCCAATA 175
Db 116 TCGCTTTTCATGAAGCAGAGGAGGATGGTCTGAACGACTTTATTTCAGAAGATTGCCAATA 175
Qy 176 ACTCTATGATGCAACACCTGAAGTTCAGTCCATTTGAAGATCTGCCAACCTCAGG 235
Db 176 ACTCTATGATGCAACACCTGAAGTTCAGTCCATTTGAAGATCTGCCAACCTCAGG 235
Qy 236 AGCTGAGCTTATGAATGCCAACCTTCTCTCCACCAAGTCTTCTCAGCAATCAACC 295
Db 236 AGCTGAGCTTATGAATGCCAACCTTCTCTCCACCAAGTCTTCTCAGCAATCAACC 295
Qy 296 TTGGCCCGTCTGCAATCTCATGCTAAACCATCTGACTTTTCACTTCTTGAAGTGTATCG 355
Db 296 TTGGCCCGTCTGCAATCTCATGCTAAACCATCTGACTTTTCACTTCTTGAAGTGTATCG 355
Qy 356 GAAAGGCGACTTTTGGAAAGGTTCTTCTAGCAAGACACAAGGCGAGAGAGTGTCTTATG 415
Db 356 GAAAGGCGACTTTTGGAAAGGTTCTTCTAGCAAGACACAAGGCGAGAGAGTGTCTTATG 415
Qy 416 CAGTCAAGTTTACAGAAAGAGCATCTCTGAAAGAAAGAGGAGAGCATATTATGT 475
Db 416 CAGTCAAGTTTACAGAAAGAGCATCTCTGAAAGAAAGAGGAGAGCATATTATGT 475

Qy 476 CGGAGCGGAATGTTCTGTTGAAGAAATGTGAAGCACCCCTTTCTGCTGGTGGGCTTTCACCTTCT 535
Db 476 CGGAGCGGAATGTTCTGTTGAAGAAATGTGAAGCACCCCTTTCTGCTGGTGGGCTTTCACCTTCT 535
Qy 536 CTTTCCAGACTGCTGACAAATTTGTTCTCTAGACTACATTAATTTGGTGGAGAGTGT 595
Db 536 CTTTCCAGACTGCTGACAAATTTGTTCTCTAGACTACATTAATTTGGTGGAGAGTGT 595
Qy 596 TCTACCATCTCCAGAGGAAACGCTGCTTCTGGAACCAACGCGGCTCGTTTCTATGCTGCTG 655
Db 596 TCTACCATCTCCAGAGGAAACGCTGCTTCTGGAACCAACGCGGCTCGTTTCTATGCTGCTG 655
Qy 656 AAATAGCCAGTGCCTTTGGGCTACCTGCAATTCATCACTGAACATCGTTTATAGAGACTTAAAC 715
Db 656 AAATAGCCAGTGCCTTTGGGCTACCTGCAATTCATCACTGAACATCGTTTATAGAGACTTAAAC 715
Qy 716 CAGAGAAATATTTGCTAGATTTCACAGGACACATTTGTTCTTACTGACTTCGGACTCTGCA 775
Db 716 CAGAGAAATATTTGCTAGATTTCACAGGACACATTTGTTCTTACTGACTTCGGACTCTGCA 775
Qy 776 AGGAGAAACATTGAACACACAGCACACATCCACCTTCTGTCGACGCGCGGAGTATCTCG 835
Db 776 AGGAGAAACATTGAACACACAGCACACATCCACCTTCTGTCGACGCGCGGAGTATCTCG 835
Qy 836 CACCTGAGGTGCTTTATAAGCAGCCTTATGACAGGACTGTGGACTGTGGTGTGCTGGGAG 895
Db 836 CACCTGAGGTGCTTTATAAGCAGCCTTATGACAGGACTGTGGACTGTGGTGTGCTGGGAG 895
Qy 896 CTGCTTTGATGAGATGCTGTATGGCTGCGGCTTTTATAGCCGAAAACACAGCTGAAA 955
Db 896 CTGCTTTGATGAGATGCTGTATGGCTGCGGCTTTTATAGCCGAAAACACAGCTGAAA 955
Qy 956 TGTACGACACATCTTGAACACAGCCTTCCAGCTGAAACCAATATTTACAAATTCGCA 1015
Db 956 TGTACGACACATCTTGAACACAGCCTTCCAGCTGAAACCAATATTTACAAATTCGCA 1015
Qy 1016 GACACCTCTCTGGAGGCGCTCTCTCAGAAAGACAGGACAAAGCGGCTCGGGGCCAAGGATG 1075
Db 1016 GACACCTCTCTGGAGGCGCTCTCTCAGAAAGACAGGACAAAGCGGCTCGGGGCCAAGGATG 1075
Qy 1076 ACTTCATGGAGATTAAGAGTATGCTTCTTCTTCTTAACTGAGATGATCTCATTA 1135
Db 1076 ACTTCATGGAGATTAAGAGTATGCTTCTTCTTCTTAACTGAGATGATCTCATTA 1135
Qy 1136 ATAAGAAATTAATCTCCCTTTTAAACCAATGTGAGTGGGCCCAACGACTTACGCACT 1195
Db 1136 ATAAGAAATTAATCTCCCTTTTAAACCAATGTGAGTGGGCCCAACGACTTACGCACT 1195
Qy 1196 TTGACCCGAGTTTACCGAAGAGCTGTCCCAACTCCATTGGCAAGTCCCTTGACAGCG 1255
Db 1196 TTGACCCGAGTTTACCGAAGAGCTGTCCCAACTCCATTGGCAAGTCCCTTGACAGCG 1255
Qy 1256 TCCTCGTCACAGCCAGCGTCAAGGAAGCTGCCGAGGCTTTCTTAGGCTTTTCTATGCGC 1315
Db 1256 TCCTCGTCACAGCCAGCGTCAAGGAAGCTGCCGAGGCTTTCTTAGGCTTTTCTATGCGC 1315
Qy 1316 CTCCACGGACTCTTTCTCTGA 1338
Db 1316 CTCCACGGACTCTTTCTCTGA 1338

RESULT 6

US-10-119-926-20
; Sequence 20, Application US/10119926
; Publication No. US20030104413A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhao, Qing A.

```
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Xu, Chongjun
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. US20030104413A1el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 789CIP2BCON
; CURRENT APPLICATION NUMBER: US/10/119,926
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 20
; LENGTH: 1456
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (217)..(1320)
US-10-119-926-20

Query Match 39.4%; Score 527.2; DB 9; Length 1456;
Best Local Similarity 69.5%; Pred. No. 1.7e-159;
Matches 734; Conservative 0; Mismatches 313; Indels 9; Gaps 1;

QY 261 TTCTCTCCACCAAGTCTTCTCAGCAATCAACCTTGGCCGCTCGTCCCAATCCTCATGC 320
DB 246 TCCACAGCCCTCCAGGCGCAATGGAACATCAACCTGGGCGCTTCAGCCAAACCAATGC 305
QY 321 TAAACCATCTGACTTTTCACTTCTTGAAGTGATCGGAAGGCGAGTTTTCGAAAGGTCT 380
DB 306 CCAGCCACCGGACTTTCACCTTCTCAAGATCATCGGAAGGNACTACGGGAAGTCT 365
QY 381 TCTAGCAAGACACAAGCGAGAGAGTGTCTATGCAAGTCAAGTTCATGAGAAAGC 440
DB 366 ACTGGCAAGCGCAAGTCTGATGGGCGTCTATGCAAGTCAAGTACTACAGAAAAGTC 425
QY 441 AATCTCAAAAAGAGAGAGAGCATATATGTCGGAGCGGAATGTTCTGTGTAAGAA 500
DB 426 CATCTTAAAGAAAGAGAGAGAGCCACATCATGCGAGAGCGCAGTGTCTTCTGAAGAA 485
QY 501 TGTGAAGCACCCCTTCTCTGTGGGCTTCACTTCTTCCAGACTGCTGACAAATGTGA 560
DB 486 CGTGGCGACCCCTTCTCTGTGGGCTTCACTTCTTCCAGACACTGGAAGCTCTA 545
QY 561 CTTTGTCTAGACTACATTAATGTGTAGAGTGTCTTACATCTCCAGAGGGAACGCTG 620
DB 546 CTTCTGTCTGACTATGTCACAGCGGAGAGCTTCTTCCACCTGAGCGGAGCGCG 605
QY 621 CTTCTCGAAGCAGCGCTGTTCTATGCTGCTGAATAGCCAGTCCCTGGCTACCT 680
DB 606 GTTCTGTGAGCCCGGCGAGGTTCTACGCTGTGAGGTGCGCAGCGCCATTTGGCTACCT 665
QY 681 GCATTCATGAACATCGTTTATAGAGACTTAAACACAGAGAATATTTTGTAGATTACCA 740
DB 666 GCATCCCTCAACATCATTTACAGGATCTGAACACAGAGACATTTCTTTGAGTGCCTA 725
QY 741 GGGACATATGTTCTTACTGACTTTGCACTCTGCAAGAGAGAACATTTGAAACACACAGCAC 800
DB 726 GGGACAGTGTGTGACGGAATTTTGGCTCTGCAAGGAAGGTGTAGAGCTTGAAGACAC 785
QY 801 AACATCCACCTTCTGTGCGCGCGGAGTATCTCGCACCTCAGGTGCTTCTATAGAGCC 860
DB 786 CACATCCACATTTCTGTGTGACCTTCTGAGTACTTGGCACCTGAAAGTCTTCGAAAGAGCC 845
QY 861 TTATGACAGGACTGTGGAGCTGGTGGCTGGAGCTGTCTTGTATGAGATGCTGTATGG 920
DB 861 TTTATGACAGGACTGTGGAGCTGGTGGCTGGAGCTGTCTTGTATGAGATGCTGTATGG 920

RESULT 7
US-09-971-118-1
; Sequence 1, Application US/09971118
; Patent No. US20020123056A1
; GENERAL INFORMATION:
; APPLICANT: DELANEY, ALLEN
; APPLICANT: YOGANATHAN, THILLAINATHAN
; TITLE OF INVENTION: SGK2 AND ITS USES
; FILE REFERENCE: KINE025CIP
; CURRENT APPLICATION NUMBER: US/09/971,118
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/21479
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/237,419
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-971-118-1

Query Match 39.4%; Score 527.2; DB 10; Length 1812;
Best Local Similarity 69.5%; Pred. No. 2e-159;
Matches 734; Conservative 0; Mismatches 313; Indels 9; Gaps 1;

QY 261 TTCTCTCCACCAAGTCTTCTCAGCAATCAACCTTGGCCGCTCGTCCCAATCCTCATGC 320
DB 117 TCCACAGCCCTCCAGGCGCAATGGAACATCAACCTGGGCGCTTCAGCCAAACCAATGC 176
QY 321 TAAACCATCTGACTTTTCACTTCTTGAAGTGATCGGAAGGCGAGTTTTCGAAAGGTCT 380
DB 177 CCAGCCACCGGACTTTCGACTTCTCTCAAGTCTCGGCAAGGGAACCTACCGGAAGGTCT 236
QY 381 TCTAGCAAGACACAAGCGAGAGAGTGTCTTATGCAAGTCAAGTTCATGAGAAAGC 440
DB 237 ACTGGCCAGCGCAAGTCTGATGGGCGTCTATGAGTGAAGTACTACAGAAAAGTC 296
QY 441 AATCTCAAAAAGAGAGAGAGCATATTTATGTCGGAGCGGAATTTCTGTGTAAGAA 500
DB 297 CATCTTAAAGAAAGAGAGAGAGCCACATCATGCGAGAGCGCAGTGTCTTCTGAAGAA 356
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Db 1454 ACCAGATGATACAGAACTTGGACACAGCATTTACAGAGAAACAGTTCATATCTGT 1513
 QY 1236 TGGCAAGTCCCTGACAGCGTCTCTGTCAGCCAGCGTCAAGAGAGCTCCGAGCTTT 1295
 Db 1514 GTGTGATCTCTGACTATTTCTATAGTGAATGCCAGTGTATTGGAGCAGATGATGATT 1573
 QY 1296 CCTAGGCTTTTCTATCGCTCCACCGGA 1325
 Db 1574 CGTTGGTTCTCTATGCACTCTCTTCAGA 1603

RESULT 9

US-10-098-841-195
 ; Sequence 195, Application US/10098841
 ; Publication No. US20020197679A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Xu, Chongjun
 ; APPLICANT: Zhou, Ping
 ; APPLICANT: Ma, Yunding
 ; APPLICANT: Wang, Jian-Rui
 ; APPLICANT: Zhao, Qing A.
 ; APPLICANT: Ren, Feiyan
 ; APPLICANT: Chen, Rui-hong
 ; APPLICANT: Wang, Dunrui
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Qian, Xiaohong B.
 ; APPLICANT: Drmanac, Radoje T.
 ; TITLE OF INVENTION: No. US20020197679A1el Nucleic Acids and
 ; FILE OF INVENTION: Polypeptides
 ; FILE REFERENCE: 784CIP2
 ; CURRENT APPLICATION NUMBER: US/10/098,841
 ; PRIOR FILING DATE: 2002-03-13
 ; PRIOR FILING DATE: 2000-06-20
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR FILING DATE: 2000-01-21
 ; NUMBER OF SEQ ID NOS: 331
 ; SOFTWARE: Pf_Fl_genes Version 1.0
 ; SEQ ID NO 195
 ; LENGTH: 2760
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (260)..(1750)
 ; US-10-098-841-195

Query Match 38.78; Score 517.2; DB 9; Length 2760;
 Best Local Similarity 68.38; Pred. No. 4.6e-156;
 Matches 717; Conservative 0; Mismatches 333; Indels 0; Gaps 0;
 QY 276 TCCTTCTCAGCAATCAACCTTGGCCGCTGCTCCAAATCTCTCATCTGCTAAACCATCTGACTT 335
 Db 685 TACTCAGACAGATCAACCTGGGACGCTGTGGAATCTCTATGCAACCACTGACTT 744
 QY 336 TCACCTCTGAAAGTATCGGAAGGCGAGTTTGGAAAGTTCTTACAGACAGACAA 395
 Db 745 TGATTTCTAAAAGTTATTGGAAGGCGAGCTTGGCAAGGTTCTTTGCAAAACGGAA 804
 QY 396 GGCAGAGAGAGTGTCTTATCAGTCAAAAGTTTACAGAGAAAGCAATCTGAAAGAA 455
 Db 805 ACTGGATGGAATTTTATGCTGTCAAGTGTACAGAAAAAATAGTTCTCAACAGAA 864
 QY 456 AGAGGAGAGCATATTATGTGCGAGCGGAATGTTCTGTGTAAGAATGTGAAGCACCTTT 515

Db 865 AGAGCAAAACATATTTATGGCTGAAAGTAAATGTGCTCTTTGAAAAATGTGAAACATCCGTT 924
 QY 516 CTGTGGGGCTTCACTTCTCTTCCAGACTGCTGACAAATGTACTCTTGTCTAGACTA 575
 Db 925 TTTGGTTGATGATATTTCTTCCAAACAACTGAAAGCTTTATTTTGTCTGGATTT 984
 QY 576 CATTAATGTTGGAGAGTGTCTTCTACCATCTCCAGAGGAAACGCTGCTTCTGTGAAACACG 635
 Db 985 TGGTTATGAGGGAGCTTTTTCACATTTACAAAGAGAAACGCTCTCTTCTGAGCACAG 1044
 QY 636 GGTCTGTTCTATGCTGCTGAAATAGCCAGTGGCTTGGGCTACCTGCTCATCTCACTGAACAT 695
 Db 1045 AGCTAGTTTACGCTGCTGAAATTTGCTAGTGCATTTGGGTACTTACATTTCCATCAAAAT 1104
 QY 696 CGTTTATAGAGACTTAAACACAGAGAAATTTTGTAGATTTCACAGGGACACATTTCTCT 755
 Db 1105 AGTATACAGAGACTTGAACACAGAAATATCTTTTGGATTCAGTAGGACATGTTGTCTT 1164
 QY 756 TACTGACTTCGGACTCTGCAAGGAGAAATTTGAACACACAGCACCAACATCCACCTTTCTG 815
 Db 1165 AACAGATTTGGGCTTTGTAAAGAGGAATTTGCTATTCTGACACCACTACACATTTTG 1224
 QY 816 TGGCAGCCGGAGTATCTCGACCTGAGTGTCTTCAAGAGAGCTTTATGACAGAGCTGT 875
 Db 1225 TGGGACACAGAGATATCTTGCACCTGAGTAAATTAGAAAAACAGCCCTATGACAATACTGT 1284
 QY 876 GGAAGTGGTGGCTGGGAGCTCTTGTATGAGATGCTGTATGGGCTCCGCTCTTTTA 935
 Db 1285 AGATGGTGGTGGCTGGGCTGTCTGTATGAAATGCTGTATGGATTTGCTCTCTTTTA 1344
 QY 936 TAGCCGAAACACAGCTGAAATGTACGACAAATTTCTGAAACAAAGCCCTCTCCAGCTGAAACC 995
 Db 1345 TTGCGAGATGTTGCTGAAATGTATGACAAATCTTTCACAAACCCCTAAGTTTGAGGCC 1404
 QY 996 AAATATTACAAATTCGCAAGACACCTCTCGAGGGCCCTCTGCAAGAGACAGACAA 1055
 Db 1405 AGAGTGTAGTCTTACAGCCTGGTCCATTTCTGGAAGAACTCTTAGAAAAAGACAGGCAAAA 1464
 QY 1056 GGGCTCGGGCCAGGATGACTTCATGAGATTAAGAGTATGATCTCTCTCTCTTAAT 1115
 Db 1465 TGACTTGTGCGCAAGAGAGCTTTCTTGAATTCAGAATCATCTCTTTTGAATCACT 1524
 QY 1116 TAACCTGGATGATCTCATTAATAAGAGATTAATCTCCCTCTTTTAAACCAAAATGTAGTGG 1175
 Db 1525 CAGCTGGCTGACCTTGTACAAAAGAGATTCACACCACTTAATCTTAATGTGCTGG 1584
 QY 1176 GCCCAACGACCTACGCACTTTGACCCCGAGTTTACGAGAGCCTGTGCCCCAACCTCAT 1235
 Db 1585 ACCAGATGATATCAGAAACTTTGACACAGCAATTTACAGAGAAACAGTTCATATTTCTGT 1644
 QY 1236 TGGCAAGTCCCTGACAGCGTCTCTGTCACAGCCAGCTCAAGGAGCTGCCGAGCTTT 1295
 Db 1645 GTGTGTATCTCTGACTATTTCTATAGTGAATGCCAGTGTATTGGAGGCAGATGATGATT 1704
 QY 1296 CTTAGGCTTTTCTCTATGCGCTCCACCGGA 1325
 Db 1705 CGTTGGTTTCTCTATGCACTCTCTTCAGA 1734

RESULT 10

US-09-925-300-860
 ; Sequence 860, Application US/09925300
 ; Patent No. US20020151681A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Craig Ruben,
 ; APPLICANT: Steve Ruben,
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA101
 ; CURRENT APPLICATION NUMBER: US/09/925,300
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270


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; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 860
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (369)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (379)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (401)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-860

Query Match      30.7%; Score 410.4; DB 10; Length 423;
Best Local Similarity 97.9%; Pred. No. 4.7e-122;
Matches 414; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 671 TGGGCTACCTGCATTCACATCAATCGTTTATAGAGACTTAAACACAGAGAAATTTTC 730
Db 1 TGGGCTACCTGCATTCACATCAATCGTTTATAGAGACTTAAACACAGAGAAATTTTC 60

QY 731 TAGATTACAGAGGACACATTCCTTACTGACTTCGGACTCTGCAAGGAGAAACATTGAAC 790
Db 61 TAGATTACAGAGGACACATTCCTTACTGACTTCGGACTCTGCAAGGAGAAACATTGAAC 120

QY 791 ACAACAGCAACATCCACCTTCTGTGGCAGCGGAGTATCTCGCACCTTGAGGTCTTC 850
Db 121 ACAACAGCAACATCCACCTTCTGTGGCAGCGGAGTATCTCGCACCTTGAGGTCTTC 180

QY 851 ATAAGCAGCTTATGACAGACTGTGACTGTGTGCTGCTGGAGCTCTTGTATGAGA 910
Db 181 ATAAGCAGCTTATGACAGACTGTGACTGTGTGCTGCTGGAGCTCTTGTATGAGA 240

QY 911 TGTGTATGCTGCTGCGCTCTTTTATAGCCGAAACACAGCTGAAATGTAGCAACATTC 970
Db 241 TGTGTATGCTGCTGCGCTCTTTTATAGCCGAAACACAGCTGAAATGTAGCAACATTC 300

QY 971 TGAACAGCTCTCCAGCTGAACCAAAATTAACAAATCCGCAAGACACTCTCTGGAGG 1030
Db 301 TGAACAGCTCTCCAGCTGAACCAAAATTAACAAATCCGCAAGACACTCTCTGGAGG 360

QY 1031 GCTCTGTCAGAGGACAGCAACAGCGCTCGGGCCAGGATGACTTCATGGAGTTA 1090
Db 361 GCTCTGTCAGAGGACAGCAACAGCGCTCGGGCCAGGATGACTTCATGGAGTTA 420

QY 1091 AGA 1093
Db 421 AGA 423

RESULT 11
US-09-918-995-15481
; Sequence 15481, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15481
; LENGTH: 447

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(447)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-15481

Query Match      28.7%; Score 383.4; DB 9; Length 447;
Best Local Similarity 97.7%; Pred. No. 2.7e-113;
Matches 387; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 943 AACACAGCTGAATGTACGACAAACATTCGAAACAAGCCTCTCCAGCTGAACCAATATT 1002
Db 32 ATCCCAAGCAGCANGNACGACAAACATTCGAAACAAGCCTCTCCAGCTGAACCAATATT 91

QY 1003 ACAAAATTCGCAAGACACACTCTCGGAGGCGCTCTCGAAGGACAGGACAAAGCGCTC 1062
Db 92 ATTAATTCGCAAGACATCTCTCGGAGGCGCTCTCGAAGGACAGGACAAAGCGCTC 151

QY 1063 GGGGCCAAGGATGACTTCATGGAGATTAAGAGTCATGCTCTTCTCTTAATTAAGTGG 1122
Db 152 GGGGCCAAGGATGACTTCATGGAGATTAAGAGTCATGCTCTTCTCTTAATTAAGTGG 211

QY 1123 GATGATCTCATTAATTAAGAGATTAATCCCTTTTAAACCAATGTAGTGGGCCCAAC 1182
Db 212 GATGATCTCATTAATTAAGAGATTAATCCCTTTTAAACCAATGTAGTGGGCCCAAC 271

QY 1183 GACCTACGGCACTTTGACCCCGAGTTTACGAGAGCGCTCTCCCACTCCATTGGCAAG 1242
Db 272 GACCTACGGCACTTTGACCCCGAGTTTACGAGAGCGCTCTCCCACTCCATTGGCAAG 331

QY 1243 TCCCTTGACAGCGCTCTCGTCACAGCAGCGTCAAGGAAAGCTCCGAGGCTTTCTTAGGC 1302
Db 332 TCCCTTGACAGCGCTCTCGTCACAGCAGCGTCAAGGAAAGCTCCGAGGCTTTCTTAGGC 391

QY 1303 TTTTCTATGCGCTCCCAAGGACTCTTCTCTGA 1338
Db 392 TTTTCTATGCGCTCCCAAGGACTCTTCTCTGA 427

RESULT 12
US-09-764-868-56
; Sequence 56, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 851
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (51)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (846)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-868-56

Query Match      26.3%; Score 351.6; DB 9; Length 851;
Best Local Similarity 66.6%; Pred. No. 8e-103;
Matches 498; Conservative 3; Mismatches 247; Indels 0; Gaps 0;
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QY 578 TTAATGCTGAGAGTTCTTCTACATCTCCAGAGGAAACGCTGCTTCTCTGGAACACGCG 637
Db 69 TTAATGAGGGGAGCTTTTTCATCTTCAAAAGAGAACGCTCTCTCTCTGAGCAGAG 128

QY 638 CTCGTTTCTATGCTGCTGAATACCCAGTGCCTTTGGGCTACCTGCAATTCACCTGAACATCG 697
Db 129 CTAGTTTTACGCTGCTGAAATGCTAGTGCATTTGGGTTACTTACATTCATCCATAAATAG 188

QY 698 TTTATAGACACTTAAACACAGAGAAATATTTTGTAGATTACAGAGGACACATTTGCTCTTA 757
Db 189 TATACAGAGACTTTGAACCCAGAAATATTTCTTTGGATTAGTAGGACATGTTGCTCTAA 248

QY 758 CTGACTTCGACCTCTGCAAGGAGAACTTGAACACACACACAAATCCACCTCTCTGTG 817
Db 249 CAGATTTTGGCTTTGTAAGAAGAAATGCTATTTCTGACACACATACCAATTTTGTG 308

QY 818 GCACGCGGAGTATCTGCACCTGAGGTGCTTCATAGCAGCCTTATGACAGACTGTGG 877
Db 309 GGACACAGAGTATCTTGCACTGAGTAATAGAAACAGCCCTATGACAACTACTGTAG 368

QY 878 ACTGGTGGCTGGGAGCTGCTTGTATGAGATGCTGTATGGCTGCGCCCTTTTATTA 937
Db 369 ATTGGTGGCTGGGCTGCTGCTATGAAATGCTGTATGGATTGCTCTCTTTTAT 428

QY 938 GCCGAAACACAGCTGAAATGTCGACAAACATTTCTGACAAAGCTCTCCAGCTGAAACCA 997
Db 429 GCCGAGATGTTGCTGAAATGTATGACAAATCTCTTCAAAACCCCTTAAGTTTGAGGCCAG 488

QY 998 ATATTACAAATTCGCAAGACACCTCTGAGGCGCTCTGCAAGAGGACAGGACAAAGC 1057
Db 489 GAGTGAGCTTTACAGCCTGGTCCATCTGGAAGACTCTCTAGAAAGAGCAGGMAAATC 548

QY 1058 GGCTCGGGGCAAGGATGACTCATGAGAGATTAGAGTATGCTCTTCTCTCTTAATTA 1117
Db 549 GACTTGTGTCGAAGGAGACTTTCTTGAATTCAGAAATCATCTCTTTTGAATCACTCA 608

QY 1118 ACTGGGATGATCTATTAATAAGAGATTACTCCCTCTTTAAACCCAAATGTGAGTGGC 1177
Db 609 GCTGGGCTGACCTTGTACAAAGAGATTCACACCACTTAATCTTAATGTGGCTGGAC 668

QY 1178 CCAACGACCTACGCACTTTGACCCGAGTTTACCGAAGAGCCTGTGCCCCAACTCCATTG 1237
Db 669 CAGATGATATCAGAACTTGTACACAGCATTTACAGAAAGAAACAGTKCCATATCTGTGT 728

QY 1238 GCAAGTCCCTGACAGGCTGCTGTACAGCCAGCTCAAGGAGCTGCGCGAGCTTTCC 1297
Db 729 GTGTATCTTCTGACTATTCTATAGTAATGCCAGWGTTATTGGAGGCAGATGATGCATTCG 788

QY 1298 TAGCCTTTCTATGCGCCTCCACGGA 1325
Db 789 TTGTTTCTTTATGCACTCTCTTCA 816

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RESULT 13

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US-09-918-995-13695
; Sequence 13695; Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13695
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(476)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-13695

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Query Match 24.1%; Score 322.8; DB 9; Length 476;

Best Local Similarity 99.4%; Pred. No. 1.1e-93; Mismatches 0; Indels 0; Gaps 0;

Matches 324; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 116 TGGCTTTTATGAGCAGAGAGGATGGGTCTGAACACTTTTATTCAGAGATTGCCAATA 175

Db 151 TGGCTTTTATGAGCAGAGAGGATGGGTCTGAACACTTTTATTCAGAGATTGCCAATA 210

QY 176 ACTCTATGATGCAACACACCTGAGTTTCACTTCTGAGATCTCCCAACCTCAGG 235

Db 211 ACTCTATGATGCAACACACCTGAGTTTCACTTCTGAGATCTCCCAACCTCAGG 270

QY 236 AGCTGAGCTTATGATGCAACACCTTCTCTCCACCAAGTCTCTCAGCAATCAACC 295

Db 271 AGCTGAGCTTATGATGCAACACCTTCTCTCCACCAAGTCTCTCAGCAATCAACC 330

QY 296 TTGGCCCGTCTGCAATCTCATGTAAACCATCTGACTTTCACTTTGAAAGTGTATG 355

Db 331 TTGGCCCGTCTGCAATCTCATGTAAACCATCTGACTTTCACTTTGAAAGTGTATG 390

QY 356 GAAAGGCGATTTTGGAAAGTCTTCTAGCAAGACACAAAGGAGTGTCTTCTATG 415

Db 391 GAAAGGCGATTTTGGAAAGTCTTCTAGCAAGACACAAAGGAGTGTCTTCTATG 450

QY 416 CAGTCAAAAGTTTACAGAAAGCA 441

Db 451 CAGTCAAAAGTTTACAGAAAGCA 476

RESULT 14

```

US-09-960-352-7426
; Sequence 7426; Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21 (10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 7426
; LENGTH: 404
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 32-LIB3058-009-Q1-K1-H7
US-09-960-352-7426

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Query Match 19.7%; Score 263.4; DB 10; Length 404;

Best Local Similarity 90.1%; Pred. No. 1.7e-74; Mismatches 282; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1026 GGAGGCGCTCTGCAAGGACAGGACAAAGCGCTCGGGCCCAAGATGACTTTCATGGA 1085

Db 12 GGAGGCGCTCTGCAAGGACAGGACAAAGCGCTCGGGCCCAAGATGACTTTCATGGA 71

QY 1086 GATTAAGAGTCACTGCTTCTCTCTTAATTAACCTGGATGATCTCATTAAATAAGAGAT 1145

Db 72 GATTAAGAGTCACTGCTTCTCTCTTAATTAACCTGGATGATCTCATTAAATAAGAGAT 131

QY 1146 TACTCCCTTTTAAACCCAAATGTAGTGGGCGCAACGACCTTACGCGACTTTGACCCCGA 1205

Db 132 TACTCCCTTTTAAACCCAAATGTAGTGGGCGCAACGACCTTACGCGACTTTTGTATCTGA 191

Qy 1206 GTTACCGAAGAGCTCTCCCACTCCATTCGAGTCCCTGACAGCGTCTCTGTAC 1265
 Db 192 GTTCACTGAAGAGCGGTCCCACTCCATTCGAGTCCCTGACAGCGTCTCTGTAC 251
 Qy 1266 AGCCAGCGTCAAGGAAGCTCCGAGGCTTCCCTAGGCTTTTCTATCGGCTCCACGGA 1325
 Db 252 AGCCAGCGTCAAGGAAGCGTGAAGGCTTCTCGGGCTTTTCTATGACCTCCCATGGA 311
 Qy 1326 CTCTTTCTCTGA 1338
 Db 312 CTCTTTCTCTGA 324

RESULT 15

US-09-918-995-10666
 ; Sequence 10666, Application US/09918995
 ; Publication No. US20030073623A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
 ; FILE REFERENCE: 20411-756
 ; CURRENT APPLICATION NUMBER: US/09/918,995
 ; CURRENT FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: US/09/235,076
 ; PRIOR FILING DATE: 1999-01-20
 ; NUMBER OF SEQ ID NOS: 38054
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 10666
 ; LENGTH: 557
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(557)
 ; OTHER INFORMATION: n = A, T, C or G
 US-09-918-995-10666

Query Match 19.5%; Score 260.8; DB 9; Length 557;
 Best Local Similarity 69.6%; Pred. No. 1.4e-73;
 Matches 352; Conservative 0; Mismatches 154; Indels 0; Gaps 0;
 Qy 340 TTCTTGAAGTATCGAAGAGCGGAGTTTGGAAAGTCTTCTAGCAAGACACAGGCA 399
 Db 50 TTTCTTAAAGTTATTGGAAGAGCGGCTTTGGCAAGGTTCTTTCGAAAACGAAACTG 109
 Qy 400 GAAGAAGTGTCTATGCAAGTCAAGTTTACAGAGAGCAATCTCTGAAAAGAGAG 459
 Db 110 GATGGAAAATTTTATGCTGTCAAGTGTACAGAAAATAATAGTTCTCAACAGAAAAGAG 169
 Qy 460 GAGAAGCATATTATGTCGAGCGGAATGTTCTGTGAAGATGTGAAGCACCTTTCTCTG 519
 Db 170 CAAAAACATATTATGGCTGAACGTATGCTCTTGAATAATGTGAACATCCGTTTTTG 229
 Qy 520 GTGGCCCTTCACTTCTCTTTCAGACTGCTGACAAATTTGTTACTTTGCTTAGACTACATT 579
 Db 230 GTTGGATTGCAATTATCTCTTCCAAACAACTGAAAAGCTTTATTTTGTCTGGATTTGTT 289
 Qy 580 AATGGTGAGAGTTGTTCTACCATCTCCAGAGGGAAGCTGCTTCTGGAACACAGGCT 639
 Db 290 AATGGAGGGAGCTTTTTTTCACCTTACAAAGAGAACGGTCTTCTGAGACAGAGCT 349
 Qy 640 CGTTTCTATGCTGAAATAGCGAGTGCCTTGGGCTACCTGCAATTCACCTGAACATCGTT 699
 Db 350 AGGTTTACGCTGCTGAATTTGCTAGTGCATTGGGTTACTTACATTCCTCAAAATAGTA 409
 Qy 700 TATAGAGACTTAAACACAGAGATATTTTCTAGATTTCACAGGACACATTTGCTTACT 759
 Db 410 TACAGAGACTTGAACCCAGAAAATATTTCTTTGGATTTCAGTAGACATGTTGCTTAAACA 469
 Qy 760 GACTTCGAGCTCTCAGAGAGACATTTGAACACACAGACACATCCACCTTCTGTGGC 819
 Db 470 GATTTTNGCTTTGTAAAGAAGGAATTTGCTATTTCTGACACCACTACCACTTTGTGGG 529

Qy 820 ACGCCGAGTATCTCGACCTGAGT 845
 Db 530 ACACCAGAGATCTTGCACCTGAAGT 555
 Search completed: June 25, 2003, 10:34:30
 Job time : 165 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1219.8	91.2	2311	2	US-08-713-709-6	Sequence 6, Appli
2	1219.8	91.2	2311	3	US-09-111-444-6	Sequence 6, Appli
3	1219.8	91.2	2311	4	US-09-541-228-6	Sequence 6, Appli
4	1218.2	91.0	2370	4	US-09-031-295-1	Sequence 1, Appli
5	255.2	13.1	2610	2	US-09-213-771-1	Sequence 1, Appli
6	255.2	19.1	2610	3	US-09-091-058-1	Sequence 1, Appli
7	248.4	18.6	1599	3	US-09-256-465-1	Sequence 1, Appli
8	248.4	18.6	1599	4	US-09-167-322-3	Sequence 3, Appli
9	241	18.0	2245	4	US-09-223-749-24	Sequence 24, Appli
10	235.4	17.6	2599	6	5266464-1	Patent No. 5266464
11	230.8	17.2	2104	4	US-09-313-930-1	Sequence 1, Appli
12	230.6	17.2	2244	3	US-09-094-714A-48	Sequence 48, Appli
13	214.6	16.0	2754	4	US-09-429-322-3	Sequence 3, Appli
14	200.2	15.0	1732	4	US-09-430-564-1	Sequence 1, Appli
15	185.6	13.9	266	1	US-08-594-031-164	Sequence 164, App
16	183.4	13.7	2549	4	US-09-467-082-3	Sequence 3, Appli
17	179.2	13.4	1637	2	US-08-966-316-10	Sequence 10, Appli
18	176.6	13.2	2196	1	US-08-313-274-1	Sequence 1, Appli
19	136.6	10.2	1890	3	US-09-289-466-2	Sequence 2, Appli
20	135	10.1	1891	3	US-09-289-466-1	Sequence 1, Appli
21	135	10.1	1929	2	US-09-016-000-10	Sequence 10, Appli
22	127.6	9.5	1276	1	US-07-688-352C-25	Sequence 25, Appli
23	127.6	9.5	1276	5	PCT-US91-02714-24	Sequence 24, Appli
24	122.2	9.1	688	4	US-08-998-416-90	Sequence 90, Appli
25	121.2	9.1	1273	2	US-08-474-379C-25	Sequence 25, Appli
26	121.2	9.1	1273	3	US-09-146-249A-25	Sequence 25, Appli
27	121.2	9.1	1273	3	US-08-206-198B-25	Sequence 25, Appli

Db 83 TCCTTTTCATGAAGCAGAGGAGGATGGTCTGAACGACTTTATTTCAGAGATTGCCAATA 142
QY 176 ACTCCTATGATGCAACACCCCTGAGTTTCAGTCCATCTTTGAGATCTCCCAACCTCAGG 235
Db 143 ACTCCTATGATGCAACACCCCTGAGTTTCAGTCCATCTTTGAGATCTCCCAACCTCAGG 202
QY 236 AGCTGAGCTTATGATGCAACCCCTCTCTCTCCACCAAGTCTCTCTCAGCAATCAACC 295
Db 203 AGCTGAGCTTATGATGCAACCCCTCTCTCTCCACCAAGTCTCTCTCAGCAATCAACC 262
QY 296 TTGGCCCGTCCGTCATCT 355
Db 263 TTGGCCCGTCCGTCATCT 322
QY 356 GAAAGGCGAGTTTGGAAAGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 415
Db 323 GAAAGGCGAGTTTGGAAAGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 382
QY 416 CAGTCAAAAGTTTACAGAAAGCAATCTCTGAAAGAAAGAGGAGGAGCATATTATGT 475
Db 383 CAGTCAAAAGTTTACAGAAAGCAATCTCTGAAAGAAAGAGGAGGAGCATATTATGT 442
QY 476 CGAGCGGAATGTTCTGTTGAAGAAATGTAAGCAACCTTTCTGGTGGGCTTTCACCTTCT 535
Db 443 CGAGCGGAATGTTCTGTTGAAGAAATGTAAGCAACCTTTCTGGTGGGCTTTCACCTTCT 502
QY 536 CTTTCCAGACTGCTGCAAAATGTAATTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 595
Db 503 CTTTCCAGACTGCTGCAAAATGTAATTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 562
QY 596 TCTACCATCTCCAGAGGAGCGTCTCTCTGAAACCAAGGCTCGTTTCTCTCTCTCTCTCTCT 655
Db 563 TCTACCATCTCCAGAGGAGCGTCTCTCTGAAACCAAGGCTCGTTTCTCTCTCTCTCTCTCT 622
QY 656 AAATAGCAGTCTGGGCTACTCTGCAATCTCACTGAACATCGTTTATAGAGACTTAAAC 715
Db 623 AAATAGCAGTCTGGGCTACTCTGCAATCTCACTGAACATCGTTTATAGAGACTTAAAC 682
QY 716 CAGAGATATTTGCTAGATTACAGGAGCACATTTGCTTCTCTCTCTCTCTCTCTCTCTCTCT 775
Db 683 CAGAGATATTTGCTAGATTACAGGAGCACATTTGCTTCTCTCTCTCTCTCTCTCTCTCTCT 742
QY 776 AGAGAAATCTTGAACACAGACACATCTCTGTCGACCGCCGAGTATCTCG 835
Db 743 AGAGAAATCTTGAACACAGACACATCTCTGTCGACCGCCGAGTATCTCG 802
QY 836 CACTGAGTCTTCTAAGCAGCCTTATGACAGGACTTGGACTGGTGGTCTGGGAG 895
Db 803 CACTGAGTCTTCTAAGCAGCCTTATGACAGGACTTGGACTGGTGGTCTGGGAG 862
QY 896 CTGCTGTATGATGATCTGTATGGCTCTGGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 955
Db 863 CTGCTGTATGATGATCTGTATGGCTCTGGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 922
QY 956 TGTACGACAACTTCTGAACAGCCTCTCCAGCTGAAACCAATATTACAAATTCGCGAA 1015
Db 923 TGTACGACAACTTCTGAACAGCCTCTCCAGCTGAAACCAATATTACAAATTCGCGAA 982
QY 1016 GACACTCTCTGGAGGCTCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1075
Db 983 GACACTCTCTGGAGGCTCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1042
QY 1076 ACTTCATGGAGATTAGAGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1135
Db 1043 ACTTCATGGAGATTAGAGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1102
QY 1136 ATAAGAGATTACT 1195
Db 1103 ATAAGAGATTACT 1162
QY 1196 TTGACCCGAGTTTACGAGAGCCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1255
Db 1163 TTGACCCGAGTTTACGAGAGCCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1222

QY 1256 TCCTCTCAGCCAGCGTCAAGAGCTGCCAGGCTTTCTTAGGCTTTTCTTAGGCTTTTCTATGCGC 1315
Db 1223 TCCTCTCAGCCAGCGTCAAGAGCTGCCAGGCTTTCTTAGGCTTTTCTTAGGCTTTTCTATGCGC 1282
QY 1316 CTCCACGCGACTCTTTCTCTCTGA 1338
Db 1283 CTCCACGCGACTCTTTCTCTCTGA 1305

RESULT 2

US-09-111-444-6
; Sequence 6, Application US/09111444
; Patent No. 6045792
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/111,444
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/712,709
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0118 US
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2311 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
US-09-111-444-6

Query Match 91.2%; Score 1219.8; DB 3; Length 2311;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1221; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 116 TGGCTTTTCATGAAGCAGAGGAGGATGGTCTGAACGACTTTATTTCAGAGATTGCCAATA 175
Db 83 TGGCTTTTCATGAAGCAGAGGAGGATGGTCTGAACGACTTTATTTCAGAGATTGCCAATA 142
QY 176 ACTCCTATGATGCAACACCCCTGAGTTTCAGTCCATCTTTGAGATCTCCCAACCTCAGG 235
Db 143 ACTCCTATGATGCAACACCCCTGAGTTTCAGTCCATCTTTGAGATCTCCCAACCTCAGG 202
QY 236 AGCTGAGCTTATGATGCAACCCCTCTCTCTCCACCAAGTCTCTCTCAGCAATCAACC 295
Db 203 AGCTGAGCTTATGATGCAACCCCTCTCTCTCCACCAAGTCTCTCTCAGCAATCAACC 262

QY 296 TTGSCCGTCTGCTCAATCTCATCTAAACCATCTGACTTTCATCTTCTTGAAGTGATCG 355
Db 263 TTGSCCGTCTGCTCAATCTCATCTAAACCATCTGACTTTCATCTTCTTGAAGTGATCG 322
QY 356 GAAAGGCGAGTTTGGAAAGGTTCTTCTAGCAACACACAAAGGCAAGAGAGTGTCTATG 415
Db 323 GAAAGGCGAGTTTGGAAAGGTTCTTCTAGCAACACACAAAGGCAAGAGAGTGTCTATG 382
QY 416 CAGTCAAGTTTACAGAGAGCAATCTGAAAAAGAGAGAGAGCAATATTATGT 475
Db 383 CAGTCAAGTTTACAGAGAGCAATCTGAAAAAGAGAGAGCAATATTATGT 442
QY 476 CGAGCGGAATGTTCTGTTGAAGATGTGAAGCACTTCTGTTGGGCTTCACTTCT 535
Db 443 CGAGCGGAATGTTCTGTTGAAGATGTGAAGCACTTCTGTTGGGCTTCACTTCT 502
QY 536 CTTTCCAGACTGCTGACAAATTTGACTTTTGTCTCTAGACTACATTAATGGTGGAGATTGT 595
Db 503 CTTTCCAGACTGCTGACAAATTTGACTTTTGTCTCTAGACTACATTAATGGTGGAGATTGT 562
QY 596 TCTACCATCTCCAGAGGAAAGCTGTTCTGGAACCAACGGGCTGTTTCTATGCTGCTG 655
Db 563 TCTACCATCTCCAGAGGAAAGCTGTTCTGGAACCAACGGGCTGTTTCTATGCTGCTG 622
QY 656 AATAGCCAGTGGCTGGGCTACCTGCAATTCAGTCACTGAACATCGTTTATAGAGACTTAAAC 715
Db 623 AATAGCCAGTGGCTGGGCTACCTGCAATTCAGTCACTGAACATCGTTTATAGAGACTTAAAC 682
QY 716 CAGAGAAATTTTGTAGATTTCAGGAGCACATTTGCTTACTGACTTCGGACTCTGCA 775
Db 683 CAGAGAAATTTTGTAGATTTCAGGAGCACATTTGCTTACTGACTTCGGACTCTGCA 742
QY 776 AGAGAAATTTTGTAGATTTCAGGAGCACATTTGCTTACTGACTTCGGACTTCG 835
Db 743 AGAGAAATTTTGTAGATTTCAGGAGCACATTTGCTTACTGACTTCGGACTTCG 802
QY 836 CACTGAGGCTTTCATAGAGCTTATGAGGAGCTTATGAGGAGCTGTTGCTGCTGGAG 895
Db 803 CACTGAGGCTTTCATAGAGCTTATGAGGAGCTTATGAGGAGCTGTTGCTGCTGGAG 862
QY 896 CTGCTTGTATGAGTCTGTATGGCTGCGCTTTTATAGCCGAAACACAGCTGAAA 955
Db 863 CTGCTTGTATGAGTCTGTATGGCTGCGCTTTTATAGCCGAAACACAGCTGAAA 922
QY 956 TGACGACAAATTTGAAACAGCTCTCCAGCTGAAACCAAAATTTACAAATTCGCA 1015
Db 923 TGACGACAAATTTGAAACAGCTCTCCAGCTGAAACCAAAATTTACAAATTCGCA 982
QY 1016 GACACTCTCGAGGGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1075
Db 983 GACACTCTCGAGGGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1042
QY 1076 ACTTCAGGAGATTAGAGTCTGTCTTCTCTCTTAACTGGAGTATCTCATTA 1135
Db 1043 ACTTCAGGAGATTAGAGTCTGTCTTCTCTCTTAACTGGAGTATCTCATTA 1102
QY 1136 ATAAGAGATTACTCCCTTTTAAACCAATGTAGTGGGCCCCAACGACTACGGCACT 1195
Db 1103 ATAAGAGATTACTCCCTTTTAAACCAATGTAGTGGGCCCCAACGACTACGGCACT 1162
QY 1196 TTGACCCGAGTTTACGAGAGAGCTGTCCCAACTCTCATTTGGCAAGTCCCTTGACAG 1255
Db 1163 TTGACCCGAGTTTACGAGAGAGCTGTCCCAACTCTCATTTGGCAAGTCCCTTGACAG 1222
QY 1256 TCCTGTTCAGAGAGAGCTGAGAGAGCTGCGAGGCTTCTAGGCTTTCTATGCTGCG 1315
Db 1223 TCCTGTTCAGAGAGAGCTGAGAGAGCTGCGAGGCTTCTAGGCTTTCTATGCTGCG 1282
QY 1316 CTCCACGAGCTCTTCTCTGA 1338
Db 1283 CTCCACGAGCTCTTCTCTGA 1305

RESULT 3

US-09-541-228-6
; Sequence 6, Application US/09541228
; Patent No. 6232077
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/541,228
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/712,709
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0118 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2311 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
; US-09-541-228-6

Query Match 91.2%; Score 1219.8; DB 4; Length 2311;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1221; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	116	TGCTTTTCATGAAGCAGAGAGGATGGTCTGAACGACTTTATTTCAGAAGATTGCCAATA	175
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QY	176	ACTCTATGCATGCAACACCCCTTCAAGTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG	235
Db	143	ACTCTATGCATGCAACACCCCTTCAAGTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG	202
QY	236	AGCTGAGCTTATGAATGCAACCCCTTCTCTCCACCAAGTCTCTTCAGCAAAATCAACC	295
Db	203	AGCTGAGCTTATGAATGCAACCCCTTCTCTCCACCAAGTCTCTTCAGCAAAATCAACC	262
QY	296	TTGGCCCGTCGTCCTCAATCTCATGTAAACCATCTGACTTTTCACTTCTTGAAGTGTATCG	355
Db	263	TTGGCCCGTCGTCCTCAATCTCATGTAAACCATCTGACTTTTCACTTCTTGAAGTGTATCG	322
QY	356	GAAAGGCGAGTTTGGAAAGGTTCTTCTAGCAACACAAAGGCAAGAGAGTGTCTTATG	415
Db	323	GAAAGGCGAGTTTGGAAAGGTTCTTCTAGCAACACAAAGGCAAGAGAGTGTCTTATG	382
QY	416	CAGTCAAGTTTACAGAGAGCAATCTGAAAAAGAGAGAGCAATATTATGT	475

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Db 383 CAGTCAAAGTTTTCAGAGAAGCAATCTGAAAAAGAGAGAGCAATATTATGT 442
Qy 476 CGGAGCGGAATGTTCTGTTGAAGATGTGAAGACACCTTTCTGGTGGGCTTCACTTCT 535
Db 443 CGGAGCGGAATGTTCTGTTGAAGATGTGAAGACACCTTTCTGGTGGGCTTCACTTCT 502
Qy 536 CTTTCCAGACTGCTGACAAATTTGACTTTTGTCTTAGACTACATTAATGTTGGAGAGTTGT 595
Db 503 CTTTCCAGACTGCTGACAAATTTGACTTTTGTCTTAGACTACATTAATGTTGGAGAGTTGT 562
Qy 596 TCTACCATCTCCAGAGGAACGCTGCTTCTGGAACCAACGCGGCTGTTTCTATGCTGCTG 655
Db 563 TCTACCATCTCCAGAGGAACGCTGCTTCTGGAACCAACGCGGCTGTTTCTATGCTGCTG 622
Qy 656 AATAGCAGCTGCTGGGTACTCTGCAATTCACCTGACATCGTTTATAGAGACTTAAAC 715
Db 623 AATAGCAGCTGCTGGGTACTCTGCAATTCACCTGACATCGTTTATAGAGACTTAAAC 682
Qy 716 CAGAGAAATATTTGCTAGATTTCAGGGACACATTTGCTTACTGACTTCGGACTCTGCA 775
Db 683 CAGAGAAATATTTGCTAGATTTCAGGGACACATTTGCTTACTGACTTCGGACTCTGCA 742
Qy 776 AGGAGAAATTTGCTAGATTTCAGGGACACATTTGCTTACTGACTTCGGACTCTGCA 835
Db 743 AGGAGAAATTTGCTAGATTTCAGGGACACATTTGCTTACTGACTTCGGACTCTGCA 802
Qy 836 CACTGAGGTGCTTCAAGCAGCTTATGACAGGACTGAGCTGGTGGTGGCTGGAG 895
Db 803 CACTGAGGTGCTTCAAGCAGCTTATGACAGGACTGAGCTGGTGGTGGCTGGAG 862
Qy 896 CTGTCTTGTATGAGATCTGTATGGCTGCGCTTTTATAGCCGAAACACAGCTGAAA 955
Db 863 CTGTCTTGTATGAGATCTGTATGGCTGCGCTTTTATAGCCGAAACACAGCTGAAA 922
Qy 956 TGTACGACAACTTCTGAAACAGCTCTCCAGCTGAAACCAAAATATTACAAATTCGCGAA 1015
Db 923 TGTACGACAACTTCTGAAACAGCTCTCCAGCTGAAACCAAAATATTACAAATTCGCGAA 982
Qy 1016 GACACTCTCGAGGGCTCTCAGAGAGGACGAGCAAGCGCTCGGGCCAGAGATG 1075
Db 983 GACACTCTCGAGGGCTCTCAGAGAGGACGAGCAAGCGCTCGGGCCAGAGATG 1042
Qy 1076 ACTTCATGAGATTAAGAGTCACTGCTTCTTCTTAAATTAAGTGGATGATCTCATTA 1135
Db 1043 ACTTCATGAGATTAAGAGTCACTGCTTCTTCTTAAATTAAGTGGATGATCTCATTA 1102
Qy 1136 ATAAGAAATTAATCTCCCTTTTAAACCAAAATGTGAGTGGGCCCCAAGCCTACGGCACT 1195
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Db 1163 TTGACCCCGAGTTTACCGAGAGCTGTCCTCCCACTCCATTTGGCAAGTCCCTGACAGCG 1222
Qy 1256 TCCTCGTCACAGCAGCTCAAGGAAGCTGCGAGGCTTTTCTAGGCTTTTCTATGCGC 1315
Db 1223 TCCTCGTCACAGCAGCTCAAGGAAGCTGCGAGGCTTTTCTAGGCTTTTCTATGCGC 1282
Qy 1316 CTCCACGAGCTCTTCTCTGTA 1338
Db 1283 CTCCACGAGCTCTTCTCTGTA 1305

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RESULT 4

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US-09-031-295-1
; Sequence 1, Application US/09031295
; Patent No. 6326181
; GENERAL INFORMATION:
; APPLICANT: LANG, Florian
; APPLICANT: WALDEGGER, Tübingen
; TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

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; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/031,295
; FILING DATE: 26-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 197-08-173.8
; FILING DATE: 28-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 058315/0123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2370 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..1335
; US-09-031-295-1

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Query Match 91.0%; Score 1218.2; DB 4; Length 2370;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 116 TGGCTTTTCATGAAGCAGAGGAGGATGGGTCTGAACGACCTTTTTCAGAGAATTCGCAATA 175
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Qy 176 ACTCTATGCTGCAACACCTCTGAGTTCAGTCCATCTTGAAGATCTCCCACTCAGG 235
Db 176 ACTCTATGCTGCAACACCTCTGAGTTCAGTCCATCTTGAAGATCTCCCACTCAGG 235
Qy 236 AGCTGAGCTTATGAATGCAACCTCTCTCCACCAAGTCTCTCAGCAAAATCAACC 295
Db 236 AGCTGAGCTTATGAATGCAACCTCTCTCCACCAAGTCTCTCAGCAAAATCAACC 295
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Qy 356 GAAAGGGCAGTTTGGAAAGGTTCTCTAGAGAGACACAAAGGAGAGAGTGTCTATG 415
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Qy 476 CGGAGCGGAATGTTCTGTTGAAGAAATGTGAAGCACCCTTTTCTGGTGGGCTTCACTTCT 535
Db 476 CGGAGCGGAATGTTCTGTTGAAGAAATGTGAAGCACCCTTTTCTGGTGGGCTTCACTTCT 535
Qy 536 CTTTCCAGACTGCTGACAAATTTGACTTTTGTCTTAGACTACATTAATGTTGGAGAGTTGT 595
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QY 656 AATATAGCAGCTGCTTGGGCTACTCTGATTCACCTGAAACATCGTTTATAGAGACTTAAAC 715
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QY 716 CAGAGAATATTTGCTAGATTCAAGGGACACATTTGTCCTTACTGACTTCGGACTCTGCA 775
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QY 776 AGGAGAACATTGAACACAGACACACATCTCTGCTGGGACCGCGGAGTATCTCG 835
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QY 896 CTGTCTTTGATGAGATGCTGTATGGGCTGCGGCTTTTATAGCCGAAACACAGCTGAAA 955
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QY 956 TGTACGACAACTTCTGAACAAGCTCTCAGCTGAAACCAAAATATTAACAAATTCGCGAA 1015
Db 956 TGTACGACAACTTCTGAACAAGCTCTCAGCTGAAACCAAAATATTAACAAATTCGCGAA 1015
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Db 1076 ACTTCATGAGATTAAGAGTCATGCTTCTTCTCTTAATTAACCTGGATGATCTCATTA 1135
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QY 1196 TTGACCCGAGTTTACCGAGAGCTGTCCCAACTCCATTGGCAAGTCCCTGACAGCG 1255
Db 1196 TTGACCCGAGTTTACCGAGAGCTGTCCCAACTCCATTGGCAAGTCCCTGACAGCG 1255
QY 1256 TCCTCGTCACAGCAGCGTCAAGGAAGCTGCCGAGGCTTTCTTAGGCTTTTCTTCTATGCCG 1315
Db 1256 TCCTCGTCACAGCAGCGTCAAGGAAGCTGCCGAGGCTTTCTTAGGCTTTTCTTCTATGCCG 1315
QY 1316 CTCCACGAGCTCTTTCTCTGA 1338
Db 1316 CTCCACGAGCTCTTTCTCTGA 1338

RESULT 5

US-09-212-771-1
; Sequence 1, Application US/09212771
; Patent No. 5958773
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-1 EXPRESSION
; FILE REFERENCE: RTS-0034
; CURRENT APPLICATION NUMBER: US/09/212,771
; CURRENT FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1641)
US-09-212-771-1

Query Match 19.1%; Score 255.2; DB 2; Length 2610;
Best Local Similarity 57.4%; Pred. No. 7e-72;
Matches 521; Conservative 0; Mismatches 378; Indels 9; Gaps 3;
QY 331 GACTTTCACTTCTTGAAGTGATCGAAAGGGCAGTTTGGAAAGGTTCTTCTAGCAAGA 390
Db 643 GAGTTTGTAGTACTGAAGCTGTGGCAAGGGCAGTTTCTGGCAAGTGATCTCTGGTGAAG 702
QY 391 CACAAGGCAAGAAAGTGTCTATGCAATCAAGTTTACAGAAAGAAAGCAATCTCTGAAA 450
Db 703 GAGAAGCCACAGGCCGCTACTACGCCATGAAGATCTCAAGNAGGAGTCACTCTGGCC 762
QY 451 AAGAAAGAGGAGACATATTATGTCGAGCCGGAATGTTCTGTGTGAAGATGTGAAGCAC 510
Db 763 AAGGACAGGTGGCCACACACTCACCGA--GAACCGCGTCTCGCAGAACTCCAGGCAC 819
QY 511 CCTTCTCTGGTGGGCTTCACTTCTTCTTCCAGAGCTGTGACAAATGTACTTTGTCTTA 570
Db 820 CCTTCTCTCACAGCCCTGAAGTACTCTTCTCCAGACCCACGACGCGCTCTGCTTTGTATG 879
QY 571 GACTACATTAATGTTGGAGAGTTGTTTACCATCTCCAGAGGGAAGCGTCTCTCTGGAA 630
Db 880 GAGTAGCCCAACGGGGGCGAGCTGTTCTTCCACCTGTCCGGGAACGTGTGTTCTCGAG 939
QY 631 CCACGGGCTCGTTTCTATGCTGCTGAAATGAGCAGTGCCTTGGGCTACCTGCAATTC--A 687
Db 940 GACCGGGCCGCTTCTATGCGCTGAGATTGTGTACGCCCTGGACTACCTGCACTCGGAG 999
QY 688 CTGAACATCGTTTATAGAGACTTAAACCCAGAGAAATATTTTGTCTAGATTCAAGGAGCAC 747
Db 1000 AAGAAGCTGTGTACCGGACCTCAAGCTGGGAACTCATGTGACAAAGGACGGGCAC 1059
QY 748 ATTGTCCTTACTGACTTCGGACTCTGCAAGGAGAACTTGAACACACAGCAACATCC 807
Db 1060 ATTAAGATCACAGACTTCGGGCTGTCAAGAGGGGATCAAGGACGGTCCACCATGAAG 1119
QY 808 ACCTTCTGTGGCAGCGGAGTATCTCGCACCTTGAGTGTCTTATGAAGCAGCCTTATGAC 867
Db 1120 ACCTTTTGGGCACACCTGAGTACCTGGCCCCCGAGGTCTGGAGGACAATGACTACGGC 1179
QY 868 AGGACTGTGAGCTGTGTGCTGGAGCTGTCTTGTATGAGATGTCTGTATGSCCTGCGC 927
Db 1180 CGTGCACTGAGTGTGTGGGCTGGGCTGTGTCATGTACGAGATGATGTGCGTCTGCTG 1239
QY 928 CTTTTTATAGCGGAACACAGCTGAAATGTAGCAACATCTCTGAACAGCCTCTCCAG 987
Db 1240 CCCTTCTCAACAGGACCATGAGAAAGCTTTTGAAGTCTATCTCTATGAGGAGATCCGC 1299
QY 988 CTGAACACCAATATTACAAATTCGCAAGACACCTCTCTGGAGGGCTCTCTGCAAGAGGAC 1047
Db 1300 TTTCCCGCGCAGCTTGGTCCCGAGGCCAAGTCTTCTGCTTTCAGGGCTGCTCAAGAGGAC 1359
QY 1048 AGGACAAAGCGGCT---CGGGCCAAAGATGATCTTATGAGAGATTAGAGTCACTGTCTC 1104
Db 1360 CCAAGCAGAGGCTTGGCGGGGCTCCGAGGACGCCAAGGAGATCATGACGATCGCTTC 1419
QY 1105 TTCTCTTAACTAACTGGGATGATCTCATTAATAGAAGATTACTCCCCCTTTTAAACCCA 1164
Db 1420 TTGCGGCTATCGTGTGGCAGCACGTTGTACGAGAAGAAAGTCTAGCCCAACCTTCAAGCCC 1479
QY 1165 AATGTAGTGGGCCCCAACACCTTACGGCACTTTGACCCCGAGTTTACCGAAGAGCCTGTC 1224
Db 1480 CAGGTACGTCGAGACTGACACAGGATTTTGTAGAGAGTTTACGCGCCAGATGATC 1539
QY 1225 CCAACTC 1232
Db 1540 ACCATCAC 1547

RESULT 6

US-09-091-058-1
; Sequence 1, Application US/09091058

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; Patent No. 6054285
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian A.
; APPLICANT: Frech, Mathias
; FILE OF INVENTION: Screening Method
; CURRENT FILING DATE: 1998-06-10
; CURRENT FILING DATE: 1998-06-10
; EARLIER APPLICATION NUMBER: PCT/EP96/04814
; EARLIER FILING DATE: 1996-11-05
; EARLIER APPLICATION NUMBER: 9525703.6
; EARLIER FILING DATE: 1995-12-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1641)
US-09-091-058-1

Query Match 19.1%; Score 255.2; DB 3; Length 2610;
Best Local Similarity 57.4%; Pred. No. 7e-72;
Matches 521; Conservative 0; Mismatches 378; Indels 9; Gaps 3;

QY 331 GACTTTCACCTTTGAAAGTGATCGGAAAGGCGAGTTTGGAAAGGTTCTTCTAGCAAGA 390
DB 643 GAGTTTGTAGTACCTGAAAGTCTGGGCAAGGCGACTTTCGCAAGGTGATCTCTGTGTAAG 702
QY 391 CACAAGGCGAGAAAGTGTCTATGTCAGTCAAAAGTTTACAGAAAGCAATCTCGAAA 450
DB 703 GAGAAAGGCGAGGCGCTACTACGCATGAAGTCTCAAGAAAGGAGTCTCGTGCC 762
QY 451 AAGAAAGGCGAGGAGCAATATATGTCGAGGCGGAATGTTCTGTTGAAGAAATGTAAGCAC 510
DB 763 AAGGACGAGGTGGCCACACACTCACCGA---GAACGCGTCTGCGAGAACTCCAGGCAC 819
QY 511 CCTTTCCTGGGCGCTTCACTTCTTTCAGAGCTCTGACAAATGTTACTTGTGCTTA 570
DB 820 CCTTTCCTGACGCGCTGAAAGTACTTCTTCCAGCCACGACGCGCTCTGCTTGTGTCATG 879
QY 571 GACTACATTAATGTGTGAGAGTGTCTTACCATCTCCAGAGGGAAGCTGCTTCTCTGAA 630
DB 880 GAGTACGCCAAGCGGGGCGAGCTGTCTTCACTGTCTCCGGAAGCTGTGTTCTCCGAG 939
QY 631 CCAGGCGCTCGTTTCTATGCTGTGAATAGCCAGTGCCTTGGGCTACCTGCAATTC---A 687
DB 940 GACCGGCGCGCTTCTATGCGCTGAGATTGTGTGACGCGCTGGAATCTGCACTCGGAG 999
QY 688 CTGAACATCGTTTATAGAGACTTAAACACAGAGAAATATTTTGTAGATTACAGGAGCAC 747
DB 1000 AAGAAACGTGTGTACCGGGACCTCAAGCTGGAGAACCTCATGCTGGCAAGGACGGGCAC 1059
QY 748 ATTGTCTCTACTGACTTTCGAGCTCTGCAAGGAGAACTTGAACACACAGCAACATCC 807
DB 1060 ATTAAGATCAAGACTTTCGGGCTGTGCAAGAGGGGATCAAGACGGTGGCCACATGAAG 1119
QY 808 ACCTTCTGTGGCAGCGCGAGTATCTCGCACCTGAGGTGCTTCTATAGCAGCCTTATGAC 867
DB 1120 ACCTTTTGGGCACACCTGAGTACCTGCGCCCGAGGTGTGGAGGACATGACTACGGC 1179
QY 868 AGNACTGTGAGCTGGTGGCTGGGAGCTGTCTTGTATGAGATGCTGTATGGCTGCGG 927
DB 1180 CGTGCAGTGGACTGTGGTGGGCTGGGCGTGTGTATGTACGAGATGATGTGCGGTGCGCTG 1239
QY 928 CCTTTTATAGCGAAACACAGCTGAAATGTAGACAACTTCTGAAAGCCTCTCCAG 987
DB 1240 CCTTCTTACACAGGACCATGAGAGCTTTTGTAGCTCATCTCTATGAGGAGATCCGC 1299
QY 988 CTGAACCAAAATTTACAAATTCGCGAAGACACCTCTCTGGAGGCGCTCTCTGCAAGAGGAC 1047
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RESULT 7

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US-09-256-465-1
; Sequence 1, Application US/09256465
; Patent No. 6043090
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION
; FILE REFERENCE: RTS-0035
; CURRENT APPLICATION NUMBER: US/09/256,465
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (88)..(1533)
US-09-256-465-1
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Query Match 18.6%; Score 248.4; DB 3; Length 1599;
Best Local Similarity 55.7%; Pred. No. 7.9e-70;
Matches 518; Conservative 0; Mismatches 406; Indels 6; Gaps 2;
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QY 330 TGACTTTCACCTTCTGAAAGTGATCGGAAAGGCGAGTTTGGAAAGGTTCTTCTAGCAAG 389
DB 537 TGACTTTCGACTATCTCAAACTCCTTGGCAAGGGAACCTTTGGCAAAAGTCATCTGTGCG 596
QY 390 ACACAAGGCGAGAAAGTGTCTATGCAAGTCAAAAGTTTACAGAAAGAAACATCTCTGAA 449
DB 597 GGAGAAGGCCACTGGCGCGCTACTACGCCATGAAGATCTCGGAAAGGAGTCATCATTCG 656
QY 450 AAGAAAGAGGAGAAAGCAATATATGTCGAGGCGGAATGTTGTTGAAGAAATGTGAAGCA 509
DB 657 CAAGGATGAAGTCGCTCACACAGTCACCGAGAGCGGGTCTCTCAGAACACC---AGGCA 713
QY 510 CCTTTCCTGGTGGGCTTCACTTCTTTCAGACTGCTGACAAATTTGACTTTTCTCT 569
DB 714 CCGTTTCTCTACCTGCGCTGAAAGTATGCTTTCAGACCCACGACCGCTGTGCTTTGTGAT 773
QY 570 AGACTACATTAATGTTGGAGAGTGTGTTACATCTCCAGAGGGAACGCTGCTTCTCTGGA 629
DB 774 GGAGTATGCCAACCGGGGTGAGCTGTCTTCCACCTGTCCCGGAGGCTGTCTTCACAGA 833
QY 630 ACCACGGGTCTGTTCTATGCTGCTGAAATAGCCAGTGTCTGGGCTAGCTGCAATTCAT 689
DB 834 GGAGCGGGCGCGGTTTATGTTGTCAGAGATTGTCTCGGCTCTTGTAGTACTTGCACCTCG 893
QY 690 GAACATCGTTTATAGAGACTTAAACACAGAGATATTTGCTAGATTTCAGAGGACACAT 749
DB 894 GGACGTGGTATACCGGACATCAAGCTGGAACCTCTATGCTGGAACAAAGATGGCACAT 953
QY 750 TGTCTTACTGACTTCCGACTCTGCAAGGAGAAACATTGAACACACAGCAACATCCAC 809
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Db 954 CAAGATCACTGACTTTGGCTCTCGAAGAGGGCATCAGTGACGGGCCACCATGAAAC 1013
Qy 810 CTTCTGTGGACCGCGAGTATCTCGCACCTGAGGTCTTCATAAGCAGCCTTATGACAG 869
Db 1014 CTTCTGTGGACCGCGAGTATCTCGCACCTGAGGTCTTCATAAGCAGCCTTATGACAG 1073
Qy 870 GACTGTGGACTGTGGTGGCTCGGAGTGTCTTGTATGAGATGCTGTATGGCTTGGCGCC 929
Db 1074 GGCGGTGACTGTGGGGCTGGGTGTGATCATGTACGAGATGATGTGGCGCGCTGCC 1133
Qy 930 TTTTATAGCGGAACACAGCTGAATGTAGCACAATCTGACAAAGCTCTCCAGCT 989
Db 1134 CTTCTCAACACGAGCAGCAGCGCTCTTGTGAGCTCATCTCATGAAAGAGATCCGCTT 1193
Qy 990 GAAACCAATATTAACAAATTCGCAAGACACCTCTCGAGGGCTCTCGAGAGGACAG 1049
Db 1194 CCGCGCAGCTGACCGCCGAGGCAAGTCCCTGCTTGTGGGTCTTAAGAGGACCC 1253
Qy 1050 GACAAAGCGCT---CGGGCCAAAGGATGATCTCATGAGATTAAGAGTCACTGTCTT 1106
Db 1254 CAAGCAGAGGCTTGGTGGGGCCCGAGCGATGCCAAGGAGTCAATGAGCAGGTTCTT 1313
Qy 1107 CTCCTTAATTAAGTGGATGATCTCATTAATAAGAAATTAAGAGTCACTGTCTT 1166
Db 1314 CTTCTCACTCACTGAGGAGGCTGCTTCCAGAAAGCTCTCGCCACCTTCAAACCTCA 1373
Qy 1167 TGTGAGTGGGCCCAACGACCTTACCGCACTTTGACCCGAGTTTACCGAAGAGCTGTCCC 1226
Db 1374 GGTACGCTCGAGGTGACACAGGTAATTCGATGATGAAATTTACCGCCAGTCCATCAC 1433
Qy 1227 CAACTCCATTGGCAAGTCCCTCGACAGCGT 1256
Db 1434 AATCACACCCCTGACCGCTATGACAGCGT 1463

RESULT 8

US-09-167-322-3
; Sequence 3, Application US/09167322
; Patent No. 6365151
; GENERAL INFORMATION:
; APPLICANT: Allegheny University of the Health
; Sciences, Halpern, Michael S.
; England, James M.
; TITLE OF INVENTION: CANCER VACCINE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorna & Monaco, P.C.
; STREET: Suite 1800, Two Penn Center Plaza
; City: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/167,322
; FILING DATE: 07-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/00582
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 7933-33 PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1599 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-167-322-3

Query Match 18.6%; Score 248.4; DB 4; Length 1599;
Best Local Similarity 55.7%; Pred. No. 7.9e-70;
Matches 518; Conservative 0; Mismatches 406; Indels 6; Gaps 2;

Qy 330 TGACTTTCACCTCTTGAAGTGTATCGAAAGGCGAGTTTGGAAAGGTTCTTCTAGCAAG 389
Db 537 TGACTTCGATATCTCAAACTCCTTGGCAAGGAACTTTTGGCAAAAGTCACTCTGTGTCG 596
Qy 390 ACACAGGAGAGAGAGTGTCTATCAGTCAAGTTTACAGAAAGAAAGCAATCCTGAA 449
Db 597 GGAAAGGCCACTGGCCGCTACTACGCCATGAAGATCTCGAAAGGAAGTCATCATTCG 656
Qy 450 AAGAAAGAGGAGGAAGCATATATGTCCGAGCGGAATGTCTGTGAAGAAATGTGAAGCA 509
Db 657 CAAGATGAAGTCGCTCACACAGTCAACGAGAGCCGGCTCTCCAGAACACC---AGGCA 713
Qy 510 CCTTTCTGTGGTGGGCTTCACTTCTTTCCAGACTGTCTGACAAATTTGPACTTTGTCT 569
Db 714 CCGCTTCTCACTGCGTGAAGTATGCTTCCAGACCCAGCAGCCGCTGTGCTTTGTGAT 773
Qy 570 AGACTACATTAATGTGGAGAGTGTCTTACCATCTCCAGAGGGAAGCGTCTTCTGGA 629
Db 774 GGAGTAGTGCACCGGGGTGAGCTGTCTTCCACCTGTCCCGGGAGCGTGTCTTCACAGA 833
Qy 630 ACCACCGGCTCGTTTCTATGCTGCTGAAATAGCAGTGTCTGGCTTACCTGATTCACCT 689
Db 834 GGAGCGGGCCCGTTTATGGTGCAGAGATTGTCTCGGCTCTTGAGTACTTGCACTCGCG 893
Qy 690 GAACATCGTTTATAGAGACTTAAACCCAGAGAAATATTTTGTAGATTTCACAGGGACACAT 749
Db 894 GGAGTGGTATACCGCGACATCAAGCTGGAAACCTCATGCTGACAAAGATGGCCACAT 953
Qy 750 TGTCTTACTGACTTCGGACTCTGCAAGGAGAACTTGAACACAAACAGCAGCAACATCCAC 809
Db 954 CAAGATCACTGACTTTGGCTCTGCAAGAGAGGCGCATCAGTGACGGGGCCACCATGAAAC 1013
Qy 810 CTTCTGTGGCAGCGCGAGTATCTCGCACCTGAGGTCTTTCATAAGCAGCCTTATGACAG 869
Db 1014 CTTCTGTGGACCGCGAGTACTCTGGCGCTGAGGTGTGGAGGACAACTGACTATGGCCG 1073
Qy 870 GACTGTGGACTGTGTGCTGGAGCTGTCTTGTATGAGATGCTGTATGGCTTGGCGCC 929
Db 1074 GGCGGTGACTGTGTGGGCTGGGTGTGATGATGACAGATGATGTGGCGCGCTGCC 1133
Qy 930 TTTTATAGCGGAACACAGCTGAATGTACGACAATCTTGAACAAAGCTCTCCAGCT 989
Db 1134 CTTCTCAACACGAGCAGCAGCGCTCTTTCGAGCTCATCTCTATGGAAGAGATCCGCTT 1193
Qy 990 GAAACCAATATTAACAAATTCGCAAGACACCTCTCGAGGGCTCTCGCAGAGGACAG 1049
Db 1194 CCGCGCAGCTGAGCGCCGAGGCGCAAGTCCCTGCTTGTGGCTGTCTTGAAGAGGACCC 1253
Qy 1050 GACAAAGCGCT---CGGGCCAAAGGATGATCTTCATGGAGATTAAGAGTCACTGTCTTCTT 1106
Db 1254 CAAGCAGAGGCTTGTGGGGGCCCGAGCGATGCCAAGAGGAGTCAATGAGCAGGTTCTT 1313
Qy 1107 CTCCTTAATTAAGTGGATGATCTCATTAATAAGAAATTAAGAGTCACTCCCGCTTTAACCCAAA 1166
Db 1314 CTTCTCAGCATCACTGGCAGGACGTTGTTCAGAAAGAGTCTCTGCCACCTTCAAACCTCA 1373
Qy 1167 TGTGAGTGGGCCCAACGACCTTACCGCACTTTGACCCGAGTTTACCGAAGAGCTGTCCC 1226
Db 1374 GGTACGCTCGAGGTGACACAGGTAATTCGATGATGAAATTTACCGCCAGTCCATCAC 1433
Qy 1227 CAACTCCATTGGCAAGTCCCTCGACAGCGT 1256

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Db 1434 AATCACACCCCTGACCGCTATGACAGCCT 1463
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RESULT 9
US-09-225-749-24
; Sequence 24, Application US/09225749
; Patent No. 6300320
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; TITLE OF INVENTION: Modulation of c-jun using inhibitors of protein kinase C
; FILE REFERENCE: ISIS3313
; CURRENT APPLICATION NUMBER: US/09/225,749
; CURRENT FILING DATE: 1999-01-05
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 2245
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (28)..(2046)
; PUBLICATION INFORMATION:
; JOURNAL: Nucleic Acids Res.
; VOLUME: 18
; ISSUE: 8
; DATE: 1990-04-25
; DATABASE ACCESSION NUMBER: X52479/Genbank
; DATABASE ENTRY DATE: 1993-09-12
US-09-225-749-24

Query Match 18.0%; Score 241; DB 4; Length 2245;
Best Local Similarity 54.9%; Pred. No. 2.5e-67;
Matches 497; Conservative 0; Mismatches 405; Indels 3; Gaps 1;

QY 274 AGTCCTTCTCAGCAATCACTTGGCCCGTCGTCGAATCCTCATGCTAAACCATCTGAC 333
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Db 982 AGTCCCTCTGAAGACAGGAACAACTTCCAAACACCTTGACCGAGTGAAACTCAACGAC 1041
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QY 334 TTTCACCTCTTGAAGTGATCGGAAGGCGAGTTTGGAAAGGTTCTTCTAGCAAGACAC 393
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Db 1042 TTCAATTTCTCATGTTGTTGGGAAGGGAGTTTGGAAAGGTGATGCTTGGCGCAGG 1101
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QY 394 AAGCAGAGAAGTGTTCTATGCAAGTCAAAAGTTTACAGAAAGAAAGCAATCTTGAAGAA 453
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Db 1102 AAGGGCAGAGAAGTGTATGCAATCAAAATCCTGAAGAGGATGTTGGTGAATTCAGGAT 1161
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QY 454 AAGAGGAGAGCAATATATGTCGGACCGGANTGTTCTTGAAGATGTTGAAGCACCCT 513
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Db 1162 GATGACGTGGAGTGACCATGGTAGAAGGAGTCTTGGCCCTGTGACAAACCCCG 1221
|||
QY 514 TTCTGTTGGCCCTTCACTTCTTTCCAGACTGCTGACAAATTTGTTACTTTGCTTAGAC 573
|||
Db 1222 TTCTGAGCAGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1281
|||
QY 574 TACATTAATGTTGAGAGTTGTTCTACCATCTCCAGAGGAAAGCTGCTTCTCTGGAACCA 633
|||
Db 1282 TATGTCACGGTGGGACCTCATGTACCAATTCAGCAAGTAGGAAATTTAAGGAACCA 1341
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QY 634 CGGCTCGTTCTATGCTGTAATAGCAGTGCCCTTGGCTACCTGCAATTCAGTGAAC 693
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Db 1342 CAAGCAGTATTTCTATGCGGAGAGATTTCCATCGGATTTCTTCTTCAATAAAGAGGA 1401
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QY 694 ATCGTTTATAGAGACTTAAACACAGAGATATTTTGTAGATTCCAGAGGACACATTTGTC 753
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Db 1402 ATCATTTATAGGATCTGAAGTTAGATACGTCATGTTGATTCAGAGGACATATCAAA 1461
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QY 754 CTTACTGACTTCGAGCTCTCAAGGAGAAATTTGAACACACACAGCAACATCAACCTTC 813
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Db 1462 ATTGCTGACTTTGGAGTGTGCAAGGAACACATGATGGATGGAGTCAAGGACGACCTTC 1521
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QY 814 TGTGGCAGCCCGAGTATCTCGACCTGAGGTGCTTATAAGCAGCCTTATCAGAGACT 873
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Db 1522 TGTGGACTCCAGATTATATCGCCAGAGATAATCGCTTATCAGCCGTATGGAATCT 1581
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QY 874 GTGACTGTGTGGCTGCTGAGCTGTCTTGTATGAGATGCTGTATGGCCTGCGCCTTTT 933
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Db 1582 GTGGACTGTGGCTTATGGCTGCTGTTGTATGAAATGCTTTCGCGGAGCCTCCATTT 1641
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QY 934 TATAGCCGAACACACAGCTGAATGTACGACCAATTTCTGAACAAGCCTCTCAGCTGAAA 993
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Db 1642 GATGTGAAGATGTAAGACAGCTATTTTCAGTCTATCATGAGACACAACTTCTCTATCCA 1701
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QY 994 CCAATATATTACAAATTTCCGCAAGACACCTCTCGAGGGCTCTCTGAGAGGACAGGACA 1053
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Db 1702 AAATCTTGTCCAGAGGCTGTCTTCTATCTGCAAGGACTGATGACCAACACACCCAGCC 1761
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QY 1054 AAGCGCT---CGGGGCCAAGGATGACTTTCATGGAGATTAAAGATCATGCTTCTTCTCC 1110
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QY 1111 TTAATTAAGTGGAGTATCTCATTAATTAAGAGATTACTCCCTTTTAAACCAATGTG 1170
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Db 1822 AGGATCGACTGGGAAAACTGGAGAACAGGAGATCCAGCCACCATTTCAAGCCCAAGTG 1881
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QY 1171 AGTGG 1175
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Db 1882 TGTGG 1886
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RESULT 10
5266464-1
; Patent No. 5266464
; APPLICANT: HOUSEY, GERARD
; TITLE OF INVENTION: METHOD OF SCREENING FOR PROTEIN INHIBITORS
; AND ACTIVATORS
; NUMBER OF SEQUENCES: 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/392,073
; FILING DATE: 10-AUG-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 154,206
; FILING DATE: 10-FEB-1988
; SEQ ID NO:1
; LENGTH: 2599
5266464-1

Query Match 17.6%; Score 235.4; DB 6; Length 2599;
Best Local Similarity 55.2%; Pred. No. 1.7e-65;
Matches 500; Conservative 0; Mismatches 401; Indels 4; Gaps 2;

QY 322 AAACCATCTGACTTTTCACTTCTTGAAGTATCGGAAGGCGAGTTTGGAAAGGTTCTT 381
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Db 1104 AAACCTGACCGATTAACTTCTCTG-TGGTGTCTGGGAAAGGCGAGCTTTGGCAAGGTCATG 1162
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QY 382 CTAGCAAGACACAAGGACAGAGAGTGTCTATGCAAGTCAAAAGTTTTACAGAAAGAGCA 441
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Db 1163 CTCTAGAGCGGAAGGTTACAGTGAACCTATGTCGCTGAAGTCTCTGAAGAAAGATGTG 1222
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QY 442 ATCTCTGAAAGAAAGAGGAGAGCAATATATGTCGAGCGGAATGTTCTGTTGAAGAAT 501
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Db 1223 GTGATCCAAGATGACCATGTGGAGTGCAATGTTGAGAGAGGTTGCTGGCCCTGCCT 1282
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QY 502 GTGAGCAGCCCTTCTCTGGTGGCCTTCACTTCTCTTTTCAGACTGCTGACAAATTTGTAC 561
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Db 1283 GGAAGCCCCCATTCCTGACTCAGCTCCATTTCTGCTTCCAGACCAATGAGCCCTCTAC 1342
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QY 562 TTGTCTTAGACTACATTAATGTTGAGAGTGTCTTCTACCATCTCCAGAGGAAACGCTGC 621
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Db 1343 TTGTGATGAGTATGTGAACGGGGGCGACCTCATGTATACATCAACAAAGTTGCGCT 1402
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QY 622 TTCTCTGGAACCAAGGCTCGTTTCTATGCTGCTGAAATAGCCAGTGCCTTTGGGCTACCTG 681
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Db 1403 TTCAAGAGGCCCATGCTGTATTTTACGCTGCAGAGATTGCCATCGGTCTTTTCTTCTTG 1462
Qy 682 CATTCACTGAACATCGTTTATAGAGACTTAAACACAGAGAATATTTTGTGTAGATTACAG 741
Db 1463 CAGAGCAAGGGCATCATTTACCGTGCCTGAACTTGAACACGTGATGCTGGATTCCGAG 1522
Qy 742 GGACACATTCCTTACTGACTCTGGAAGTCTGCAGAGAGAACATTTGAACACACAGCACA 801
Db 1523 GGGCACATCAAAATCGCTGCTTGTGGCATGTCTAAAGAGAAATATCTGGGATGGGTGACA 1582
Qy 802 ACATCCACCTTCTGTGACGCGCGAGTATCTCGCACCTGAGTGTCTTCAATAGCAGCCT 861
Db 1583 ACCAAGACATCTGTGCACTCCAGACTCAATTTGCCCCAGAGATCAATGCTTATCAGCCC 1642
Qy 862 TATGACAGGACTGTGGACTGTGCTGCTGGAGCTGTCTTGTATGAGATGCTGTATGGC 921
Db 1643 TAGGAAAGTCTGTGGACTGTGGCGTGTGGAGTCTGCTGTATGAAATGTTGGCTGGC 1702
Qy 922 CTGCGGCTTTTATAGCCGAAACACAGCTGAATGTACGACACATCTTGAACAGCCT 981
Db 1703 CAGGCACCTTTTGAAGGGAGGATGAGGATGAATCTTCCAGTCAATCATGGAGCACAAC 1762
Qy 982 CTCAGCTGAACCAATATTTACAAATTCGCAAGACACCTCTCGAGGGCCTCCTGCAG 1041
Db 1763 GTGGCTATCCCAAGTCCATGTCTAAGAAAGCTGTGGCAATCTGCAAGGGCTTAATGACC 1822
Qy 1042 AAGGACAGGACAAAGCGGCTCG---GGGCCAAGGATGACTTCATGGAGATTAAGAGTCA 1098
Db 1823 AAACACCCAGGACGCGCTGGTGTGGCGCTGAAGGGACGAGACATTAAGAGCAT 1882
Qy 1099 GTCTTCTTCTTAATTAATCTGGATGATCTCAATTAATGAAGAGATTAATCTCCCGCTTT 1158
Db 1883 GCATTTTTCGGTATATCGACTCGGAGAACTCGAAGCAAGGAGATTCAGCCACCGTAT 1942
Qy 1159 AACCCAAATCGATGGGCCCCAACGACCTACGGCCTTTGACCCCGAGTTTACCGAAGAG 1218
Db 1943 AAACCAAAAGCTAGAGACAAAGCAGACACCTCCAACCTTCACAAAGAGTTTCACAGGC 2002
Qy 1219 CCTGT 1223
Db 2003 CCTGT 2007
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RESULT 11
US-09-313-930-1
; Sequence 1, Application US/09313930
; Patent No. 6235723
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of Human Protein
; TITLE OF INVENTION: Kinase C-delta Expression
; FILE REFERENCE: ISPH-0357
; CURRENT APPLICATION NUMBER: US/09/313,930
; CURRENT FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2104
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (59)..(2089)
; PUBLICATION INFORMATION:
; AUTHORS: Aris, J. P.
; AUTHORS: Basta, P. V.
; AUTHORS: Holmes, W. D.
; AUTHORS: Ballas, L. M.
; AUTHORS: Moomaw, C.
; AUTHORS: Rankl, N. B.
; AUTHORS: Blobel, G.
; AUTHORS: Loomis, C. R.
; AUTHORS: Burns, D. J.
```

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; TITLE: Molecular and biochemical characterization of a
; TITLE: recombinant human PKC-delta family member
; JOURNAL: Biochim. Biophys. Acta
; VOLUME: 1174
; ISSUE: 2
; PAGES: 171-181
; DATE: 1993-08-19
; DATABASE ACCESSION NUMBER: L07860
; DATABASE ENTRY DATE: 1993-11-02
; US-09-313-930-1

Query Match 17.2%; Score 230.8; DB 4; Length 2104;
Best Local Similarity 54.4%; Pred. No. 4.6e-64;
Matches 491; Conservative 0; Mismatches 402; Indels 9; Gaps 1;

Qy 332 ACTTTCACCTTCTTGAAGTGATCGGAAAGGGCAGTTTTCGAAAGGTTTCTTCTAGCAAGAC 391
Db 1101 ACTTTCATCTTCCACAAGTCTCGGCAAGGAGCTTCGGAAAGGTTGCTGCTGGAGAGC 1160
Qy 392 ACAAGCAGAAGAAGTGTCTATGCAGTCAAAAGTTTTCAGAGAAGAAAGCAATCCTGAAAA 451
Db 1161 TGAAGGGCAGAGAGAGATCTCTGCCATCAAGGCCCTCAAGAGGATGTGGTCTGATCG 1220
Qy 452 AGAAGAGAGAGAGACATATTTATGTCGAGGGGAATGTTCTGTTGAAGAATGTGAAGCACC 511
Db 1221 ACACACAGCTGGAGTGCACCATGTTTGAAGCGGTGCTGCACACTTGCAGCAGAGAAATC 1280
Qy 512 CTTTCTCTGTGGCGCTTCACTTCTTTCAGACTGCTGACAAATTTGTAATTTTGTCTCTAG 571
Db 1281 CTTTCTCACCCACCTCATCTGCACCTTCCAGACCAAGACCACTGTTCTTTTGTATGG 1340
Qy 572 ACTACATTAATGTTGGAGAGTTGTTCTACCATCTCCAGAGGGAACGCTGCTTCTCGAAC 631
Db 1341 AGTTCCTCAACGGGGGACCTGATGTACCATCCAGACAAAGCGCGCTTTGAACTCT 1400
Qy 632 CAGGGCTCGTTTCTATGCTGTAATAAGCAGTGCCTTGGGCTACCTGATCTACTGA 691
Db 1401 ACCGTGCCACGTTTATGCGCTGAGATAATGTGTGGACTGTCAGTGTTCACAGCAAGG 1460
Qy 692 ACATCGTTTATAGAGACTTAAACACAGAGATAATTTTGTAGATTTCACAGGGACACATTG 751
Db 1461 GCATCATTTACAGGGACCTCAAACTGGACAATGTGCTGTTGGACCGGGATGGCCACATCA 1520
Qy 752 TCCTTACTGAGTTTCGAGCTCTGCAAGGAGAAACATTTGAACACACAGCACAACATCCACCT 811
Db 1521 AGATTGCCGACTTTGGGATGTGCAAGAGAAATATTCGGGAGAGCCGGCCGAGACCT 1580
Qy 812 TCTGTGGCACCGCGGAGTATCTGCACCTGAGTGTCTTCAATAGCAGCTTATGACAGGA 871
Db 1581 TCTGCGCACCCCTGACTATATCGCCCTGAGATCTTACAGGGCTTGAAGTACACATCT 1640
Qy 872 CTGTGAGCTGTTGTCCTGGGAGCTGTTCTGTATGAGATGCTGTATGGCTGCCGCTT 931
Db 1641 CTGTGAGCTGTTGTTCTTTCGGGGTCTTCTGTGACAGATGCTCATTTGAGCAGTCCCT 1700
Qy 932 TTTATAGCCGAAACACAGCTGAAATGTACGACAACATTTCTGAACAAGCTCTCCAGCTGA 991
Db 1701 TCCATGCTGATGAGGATGAATCTTTCGAGTCCATCCGTGTGGACAGCCACATATTC 1760
Qy 992 AACCAAAATTTACAAATTCGCAAGACACCTCTGAGGGCTCTCTGCAAGAGGACAGGA 1051
Db 1761 CCGCTGGATCACCAAGGAGTCCAAGGACATCTGAGAAAGCTCTTTGAAGGAAACCA 1820
Qy 1052 CAAAGCGCTCGGGCCCAAGGATGCTTTCATGGAGTTAAGAGTATGTTCTTCTCTCT 1111
Db 1821 CCAAGAGGCTGGGAATGACGGGAAAC-----ATCAAAATCCACCCCTCTTCTCAAGA 1871
Qy 1112 TAATTAACCTGGGATGATCTCATTAAAGAAAGATTACTCCCCCTTTTAAACCCAAATGTGA 1171
Db 1872 CCATAAATCTGACTCTGCTGGAAAGCGGAGGTTGGAGCCACCCCTTCAGGCCCAAGTGA 1931
Qy 1172 GTGGGCCCAACGACCTTACGGCCTTTTGACCCCGAGTTTACCGAAGAGCTGTGCCCAACT 1231
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Db 1932 AGTCAACAGAGACTACAGTAACCTTTGACAGGAGTTCTGTAACGAGAGCGCGCTCT 1991
QY 1232 CC 1233
Db 1992 CC 1993

RESULT 12

US-09-094-714A-48
; Sequence 48, Application US/09094714A
; Patent No. 6117847
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett, Nicholas M. Dean
; TITLE OF INVENTION: OLIGONUCLEOTIDES FOR ENHANCED MODULATION OF
; TITLE OF INVENTION: PROTEIN KINASE C EXPRESSION
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6117847ris, LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/094,714A
; FILING DATE: June 15, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/601,269
; FILING DATE: 14-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/478,178
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/089,996
; FILING DATE: 09-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/852,852
; FILING DATE: 16-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-2943
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2244
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-094-714A-48

Query Match 17.2%; Score 230.6; DB 3; Length 2244;
Best Local Similarity 54.9%; Pred. No. 5.6e-64;
Matches 497; Conservative 0; Mismatches 404; Indels 4; Gaps 2;
QY 274 AGTCTTCTCAGCAATCAACCTTGGCCGCTGCTCCATCTCATGCTAAACCATCTGAC 333
Db 982 AGTCCCTCTGAAGCAGCAACAACTTCCAAACAACTTGACCGAGTGAACCTCAGCGAC 1041
QY 334 TTTCACCTCTTGAAGGATGATCGGAAGCGAGTTTGGAAAGTTCTTCTAGCAAGACAC 393
Db 1042 TTCAATTTCTCATGGTGTGGGAGGAGTTTGGAAAGGTGATGCTTTCGCGACAG 1101
QY 394 AAGCAGAGAAGTGTCTTATGTCAGTCAAAAGTTTATCAGAGAAGCAATCTCTGAAAG 453

Db 1102 AAGGGCACAGAAAGACTGTATGCAATCAAAATCTCGAAGAGGATGTGTGATTCCAGGAT 1161
QY 454 AAAGAGGAGAAGCATATTATGTCGGAGCGGAATGTTCTGTTGAGAAATGTGAAGCACCTT 513
Db 1162 GATGACGTGGAGTGCACCATGGTAGAAAAGCGAGTCTTGGCCCTGCTTGACAAACCCCG 1221
QY 514 TTCTCTGGTGGCCTTCCACTTCTCTTTCCAGAGTGTCTGACAAATTTGTACTTTGTCTAGAC 573
Db 1222 TTCTTGACGAGCTGCACCTCTGCTTCCAGACAGTGGATCGGCTGTACTTCTGTCATGGA 1281
QY 574 TACATTAATGGTGGAGATTGTTTACCATCTCCAGAGGGAACGCTGCTTCTCTGGAACCA 633
Db 1282 TATGTCACCGTGGGACCTCATGTACCAATTTACAGAAAGTAGAAAAATTTAAGGAACCA 1341
QY 634 CGGCTCGTTTCTATGCTCTGAAATAGCAGTGCCTTGGGCTACCTGCTGCTTCTGCTGAAC 693
Db 1342 CAAGCAGTATTCTATGCGGCGAGATTTCATCGGATTGTTCTTCTTCTATAAAGAGGA 1401
QY 694 ATCGTTTATAGAGACTTAAACCCAGAGAAATATTTCTAGATTTCACAGGAGACATTTGTC 753
Db 1402 ATCAATTAAGGATCTGAATAGATTAACGTCATGTTGGATTTCAGAGAGACATATCAA 1461
QY 754 CTTACTGACTTCGGACTCTGCAAGGAGAAATGTAACAACAACAGACAAATCCACTTC 813
Db 1462 ATTGCTGACTTTGGGATGTCAAGGAAACACATGATGGATGGAGTCAAGACGAGCTTC 1521
QY 814 TGTGGCACCGCGAGTATCTCGCACTGAGGTGCTTTCATAAGCAGGCTTATGACAGGACT 873
Db 1522 TGTGGGACTCCAGATTATATCGCCCGAGAGATAATCGCTTATCAGCCGTATGGAAATCT 1581
QY 874 GTGGACTGTGTGCTGCGGAGCTGTCTTGTATGAGATGCTGTATGGCCTGCGCGCTTTT 933
Db 1582 GTGGACTGTGGCCTATGCGCTCTGTTGTATGAATGCTTTCGCGGAGCTTCATTT 1641
QY 934 TATAGCCGAAACACAGCTCAAAATGTACGACAAATTTCTGAACAAGCTTCTCCAGCTGAAA 993
Db 1642 GATGTTGAAGATGAAGACGAGCTATTTCAGTCTATCATGGAGCACACGTTTCTATCCA 1701
QY 994 CCAATATTACAATTTCCCAAGACACCTCTCGAGGGCTCTGCGAGAGGAGGACGA 1053
Db 1702 AAATCTTGTCCAAGGAGCTGTTTCTATCTGCAAGGAGTGTATGACCAACACCCAGCC 1761
QY 1054 AAGCGCT---CGGGGCCAAGGATGACTTTCATGGAGATTAAAGAGTCTGTTCTTCTCC 1110
Db 1762 AAGCGCTGGCTGTGGGCTGAGGGGAGAGGAGCTGAGAGAGATGCTTCTTCTCCG 1821
QY 1111 TTAATTAAGTGGAGTATCTCAATTAATAAGAGATTAATCTCCCTTTTAAACCAAAATGT 1170
Db 1822 AGGATCGACTGGA-AAACTGGAGAACAGGAGATCCAGCCACCAATTCAAGCCCAAGTG 1880
QY 1171 AGTGG 1175
Db 1881 TGTGG 1885

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US-09-429-322-3
; Sequence 3, Application US/09429322A
; Patent No. 6190869
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN KINASE C-THETA
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0100
; CURRENT APPLICATION NUMBER: US/09/429,322A
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 3
; LENGTH: 2754
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: (95)..(2215)
US-09-429-322-3

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Query Match	15.0%	Score 214.6	DB 4	Length 2754
Best Local Similarity	52.3%	Pred. No. 9.5e-59		
Matches 503	Conservative 0	Mismatches 449	Indels 9	Gaps 1
Qy	281	CTCAGCAAAATCAACACTTTGGCCGTCGTCCAAATCTCATGCTAAACCATCTGACTTTCAC	340	
Db	1179	CTGNACTGACACAAAGAAAGACCATCTCTGCAGATTAAACTAAAAATTTGAGGATTTTATCT	1238	
Qy	341	TCITTGAAAGTGATCGGAAAGGGCAGTTTTTGGAAAGGTTCTTCTAGCAAGACACAAGCAG	400	
Db	1239	TGCACAAAATGTTGGGGAAAGGAAGTTTTGGCAAGGTCCTCTGCGCAGAAATTCGAAGAAA	1298	
Qy	401	AAGAAGTGTTCTATGTCAGTCAAAAGTTTTTACAGAGAAAGCAATCCTCGAAAAGAAAGAGG	460	
Db	1299	CCAATCAATTTTTTCGCAATTAAGGCCCTTAAGAAAAGATGTGGTCTTGATGGACGATGATG	1358	
Qy	461	AGAAGCATATTAATGTCGGAGCGGAATGTCTGTGTTGAAGAATGTGAAGCAACCCCTTTCCTGG	520	
Db	1359	TTGAGTGCACGATGGTAGAAGAGAGTTCTTCTCTTGGCTGGGAGCATCCGTTTCTGA	1418	
Qy	521	TGGCCCTTCACTCTCTTTCAGACTCGTGCACAAATTTGTACTTTGTCTTCTAGACTACATTA	580	
Db	1419	CGCACATGTTTTGTACATTTTCAGACCAGGAAAAACCTCTTTTTTGTGATGGAGTACCTCA	1478	
Qy	581	ATGTGTGAGAGTTGCTTCTACCATCTCCAGAGGGAACGCTGCTTCTCGAACCCACGCGCTC	640	
Db	1479	ACGGAGGGGACTTAATGTATCCACATCCAAAGCTGCCAAGTTTCGACCTTTCAGAGCGA	1538	
Qy	641	GTTTCTATGCTGTGAAATAGCCAGTGCCTTGGGCTACCTGCATTCACAGCAATCGTTT	700	
Db	1539	CGTTTTATGCTGTGAAATCAATCTTGCTGTGCAAGTTTCTTCAATTCAAAAGGAATAGTCT	1598	
Qy	701	ATAGAGACTTTAAACACAGAGAAATTTTGCTAGATTACAGGGGACACATTTGCTTACTG	760	
Db	1599	ACGGGACCTGAAGCTAGATAACATCTGTTTAGACAAAGATGGACATATCAAGATTCGGG	1658	
Qy	761	ACTTTCGACCTCTGCAAGGAGAACTTTGAAACACACAGCACAAACATCCACCTTCTGTGGCA	820	
Db	1659	ATTTTGGATGTGCAAGGAGAACATGTTAGGAGATGCCAGACGAATACCTTCTGTGGGA	1718	
Qy	821	CGCCGGAGTATCTCGACCTGAGGTGCTTCATTAAGCAGCCTTATGACAGACTGTGGACT	880	
Db	1719	CACCTGACTACATCGCCCCAGAGATCTTGCTGGGTGAGAAATCAACACCACTCTGTGACT	1778	
Qy	881	GGTGGTCCCTGGGAGCTGCTTTGTATGAGATGCTGTATGGCTTCGCCCTTTTATAGCC	940	
Db	1779	GGTGGTCTTCGGGGTCTCTCTTTATGAATGCTGATTTGGTCACTGCGCTTTTCCACGGC	1838	
Qy	941	GAACACACAGCTGAAATGTACGACAAACATTTGAAACAAGCCCTCTCCAGCTGAAACCAATA	1000	
Db	1839	AGGATAGGAGGAGCTCTTCACCTCCATCCGATGGACAATCCCTTTTACCACGGTGGC	1898	
Qy	1001	TTACAAATTCGGCAAGACACCTCTCGAGGGCCTCTGACAGAGGACAGGACAAAGCGGC	1060	
Db	1899	TGGAGAAGGAAGCAAGACCTCTGTGTAAGCTCTTCGTGCGAGAACCTGTAGAAAGAGC	1958	
Qy	1061	TCGGGGCCAAAGGATGACTTTCATGGAGATTAAAGTGCATGCTTCTCTCTCTTAATTAAC	1120	
Db	1959	TGGCGTGGGGGAGACATCCGCCAG-----CACCCCTTTGTTTCGGGAGATCAACT	2009	
Qy	1121	GGGATGATCTCATTAATAAGAAAGATTACTCCCCCTTTTAAACCCAAATGTGTAGTGGGCCA	1180	
Db	2010	GGGAGGAACCTTGAAACGGAAGGAGATTGACCCACCGCTTCGGGCCGAAAGTGAATACCAT	2069	
Qy	1181	ACGACCTACGCGACTTTTGACCCCGAGTTTACCGAAGAGCCTGTCCCAACTCCATTCGCA	1240	
Db	2070	TTGACTCGACGAATTTTCGACAAAGAAATCTTTAAACGAGAAAGCCCGCGTGTCAATTCGCG	2129	
Qy	1241	A	1241	

Db 2130 A 2130

RESULT 14

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US-09-430-564-1
; Sequence 1, Application`US/09430564
; Patent No. 6372467
; GENERAL INFORMATION:
; APPLICANT: John Blenis
; APPLICANT: Kay K. Lee-Fruman
; APPLICANT: Calvin J. Kuo
; TITLE OF INVENTION: P54S6K AND P85S6K GENES, PROTEINS,
; TITLE OF INVENTION: PRIMERS, PROBES, AND DETECTION METHODS
; FILE REFERENCE: 00246/S06002
; CURRENT APPLICATION NUMBER: US/09/430,564
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/106,141
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-430-564-1

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Query Match	15.0%	Score 200.2	DB 4	Length 1732
Best Local Similarity	53.9%	Pred. No. 3.1e-54		
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Gaps	1			
Qy	410	TCATGTCAGTCAAAGTTTACAGAGAAGAAACAATCCTGAAAAGAAAGAGGAGGAAGCAT	469	
Db	319	TATATGGCATGAAGTCTCTAAGGAAGCCAAAATTTGCGCAATGCCAAGACACAGCAC	378	
Qy	470	TTATGTGCGAGCGGAATGTTCTGTGAAGAATGTGAAGCACCCCTTTCTCGTGGCGCCTTC	529	
Db	379	ACACACGGGCTGAGCGGAACATTTCTAGAGTCAGTGAAGCACCCCTTTATTGTGGAAC	438	
Qy	530	ACTTCTCTTTCCAGACTGTGCACAAATTTGACTTTGTCTTAGACTACATTAATGGTGGAG	589	
Db	439	CCTATGCTTTCCAGACTGGTGGCAAACTCTACCTCATCTCTTGATGGCTCAGTGGTGGCG	498	
Qy	590	AGTTGTTCTACCATCTCCAGAGGAAACGCTGCTTCTGGAACCAACGGGCTCGTTTCTATG	649	
Db	499	AGCTCTTACGCACTGGACGAGAGGGCACTTCTCTGGAAGATACGGCCTGCTTCTATCC	558	
Qy	650	CTGCTGAATPAGCCAGTGCCTTGGGCTPACCTGCATCTCACTGAACATCGTTTATAGAGACT	709	
Db	559	TGGCTGAGATCACTGCGCCCTGGCCATCTCCACTCCCAAGGCATCATCTACCGGGACC	618	
Qy	710	TAAACACAGAGATATTTTGTCTAGATTCACAGGGACACATTTGCTTACTTGACTTCGGAC	769	
Db	619	TCAAGCCGAGAACATCATGCTCTCAGCAGCCAGGGCCACATCAAACCTGACCGACTTTGGAC	678	
Qy	770	TCTGCAAGGAGAACATTGAAACAAACAGCACAACTCCACCTTCTGTGGCACCGCGAGT	829	
Db	679	TCTGCAAGGAGTCTATCCATGAGGGCGGCTCACTCACCTTCTGCGGCACCATTTGAGT	738	
Qy	830	ATCTCGCACCTGAGGTGCTTTATGAAGCAGCCTTTATGACAGGACTGTGGACTGTGTGGCC	889	
Db	739	ACATGGCCCTCGAGATTCTGTCGCGAGTGGCCACAAACCGGGCTGTGGAATGTTGGAGCC	798	
Qy	890	TGGGAGCTGTGTTGATAGATGCTGTATGGCCCTGGCCCTTTTATAGCGGAACACACAG	949	
Db	799	TGGGGGCCCTGATGTACGACATGCTCACTGGATTCGGCCCTTTTACCGCAGAGAAACCGGA	858	
Qy	950	CTGAAATGTACGACAAACATTTCTGAACAAGCCTCTCCAGCTGAAACCAAATATTACAAATT	1009	
Db	859	AGAAAACCATGGATTAAGATCATCAGGGCAAGCTGGCACTTGCCCCCTCACTCACCCACG	918	
Qy	1010	CCGCAAGACACCTCTCTGGAGGGCCTCTCTGAGAAGGACAGGACAAAGCGCTCGGG--G	1066	

Db 919 ATGCCGGGACCTTGTCAAAAGTTTCTGAAACGGAATCCAGCCAGCGGATTGGGGTG 978
 Qy 1067 CCAAGGATGACTTCATGAGATTAAAGATCATGTCTTCTCTTAATTAACCTGGGATG 1126
 Db 979 GCCAGGGGATGCTGTGATGTGAGAGACATCCCTTTTCCGGCAGATGAATTGGGACG 1038
 Qy 1127 ATCTCATTAATAAGAGATTACTCCCGCTTTTAACCCAAATGTGAGTGGGCCCAACGACC 1186
 Db 1039 ACCTTGTGCTGGCGTGTGACGCCCTTTTCAGGCCCTGTCTGCAGTCAGAGGAGGACG 1098
 Qy 1187 TACGGCACTTTGACCCCGAGTTTAC 1211
 Db 1099 TGAGCCAGTTTGATACCCGCTTCAC 1123

RESULT 15

US-08-594-031-164
 ; Sequence 164, Application US/08594031
 ; Patent No. 5783182
 ; GENERAL INFORMATION:
 ; APPLICANT: THOMPSON, Timothy C.
 ; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
 ; NUMBER OF SEQUENCES: 175
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BAKER & BOTTS, L.L.P.
 ; STREET: 1299 Pennsylvania Avenue, N.W.
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20004-2400
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/594,031
 ; FILING DATE: 30-JAN-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/006,838
 ; FILING DATE: 16-NOV-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Remenick, James
 ; REGISTRATION NUMBER: 36,902
 ; REFERENCE/DOCKET NUMBER: 0A146-0110
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-639-7700
 ; TELEFAX: 202-639-7890
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 164:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 266 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE:
 ; ORIGINAL SOURCE:
 ; US-08-594-031-164

Query Match 13.9%; Score 185.6; DB 1; Length 266;
 Best Local Similarity 91.2%; Pred. No. 4.5e-50;
 Matches 219; Conservative 0; Mismatches 19; Indels 2; Gaps 2;
 Qy 320 CTAACCATCTGACTTTTCACTTCTTGAAGTATCGGAAGGCGAGTTTGGAAAGGTTTC 379
 Db 29 CCAAACTCTCGACTTTCCTTCTTG-AAATGATCGGAAGGCGAGTTTGGAAAGGTTTC 87
 Qy 380 TTCTAGCAACACAAAGCGGAGAGAGTGTCTATGCAGTCAAAGTTTTCACAGAAAG 439

Db 88 TTCTGGCTAGGCACAAGGCGAGAAAGTATTCTATGCAGTCAAAGTTTTCACAGAAG-AAG 146
 Qy 440 CAATCCTGAAAAAGAAAGAGGAGAGCATATTATGTCCGAGCGGAATGTTCTGTTGAAGA 499
 Db 147 CCATCCTGAAGAAAGAAAGGAGAGCATATTATGTCAAGAGCGGAATGTTCTGTTGAAGA 206
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 Db 207 ATGTGAAGCACCCCTTTTCTGTTGGGCTTTCACCTTCTTTCAGAGTGTGACAAAGTCT 266

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 Job time : 66 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 05:48:04 ; Search time 239 Seconds
(without alignments)
12607.422 Million cell updates/sec

Title: US-10-067-977-1

Perfect score: 1338

Sequence: 1 atggggagatgcaggcgc.....ccacggactcttctctga 1338

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Searched: 2185239 seqs, 1125995159 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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13: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
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19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1219.8	91.2	2311	19	AAV23833 Human protein kina
2	1218.2	91.0	1296	22	AAF44639 Novel protein kina
3	1218.2	91.0	2346	19	AAV74190 Human sgk DNA. Ho
4	1218.2	91.0	2370	19	AAV48311 Human cell-volume
5	1218.2	91.0	2370	24	ABK84749 Human cDNA differe
6	1218.2	91.0	2370	24	ABN97360 Gene #3858 used to
7	1218.2	91.0	2370	24	ABL70006 Pancreas cancer re
8	1144	85.5	2281	20	AAZ33647 Human breast tumou
9	983	73.5	2365	21	AAA46592 DNA encoding a rat

10	978.8	73.2	2432	22	AAF44640 Novel protein kina
11	527.2	39.4	1366	22	AA544987 cDNA encoding nove
12	527.2	39.4	1812	22	AAF44737 Novel protein kina
13	527.2	39.4	1812	24	AAD36141 Human serum and g1
14	527.2	39.4	1834	21	AA227856 Human serum and g1
15	527.2	39.4	2146	21	AA227857 Human serum and g1
16	520.4	38.9	2404	21	AA227858 Human serum and g1
17	520.4	38.9	2512	20	AAV99653 Human serum glucoc
18	520.4	38.9	2572	23	ABK43712 DNA encoding novel
19	520.4	38.9	2702	23	ABK43558 DNA encoding novel
20	520.4	38.9	2711	22	AA159776 Human polynucleoti
21	517.2	38.7	2760	22	AA157990 Human polynucleoti
22	516.2	38.6	1333	22	AAH99535 Human protein enco
23	515.6	38.5	3019	21	AAAG9248 Human serine thro
24	410.4	30.7	423	21	AAF16425 Human prostate can
25	356.2	26.6	1346	22	AAF44641 Novel protein kina
26	351.6	26.3	851	22	AA527021 cDNA encoding nove
27	351.6	26.3	851	23	ABK43988 DNA encoding nove
28	348.8	26.1	2483	22	AAK94684 Human full-length
29	306.4	22.9	449	21	AAC03936 Human secreted pro
30	283.8	21.2	2375	23	ABL19107 Drosophila melanog
31	283.8	21.2	2425	23	ABL28911 Human colon specif
32	283.8	21.2	3872	24	ABA91312 Human protein kina
33	282.4	21.1	2250	22	AAF44642 Novel type murine A
34	259.4	19.4	2626	21	AA09078 Mouse Akt cDNA. M
35	259.4	19.4	2626	24	AAAD28550 Human Akt-3 coding
36	258.8	19.3	1440	21	AAAG2451 Human Akt3 encodin
37	258.8	19.3	1440	24	ABL50839 Human Akt-3 nucleo
38	258.8	19.3	1547	21	AAAG2450 DNA encoding a hum
39	258.8	19.3	1570	21	AAAG6637 Human Akt3 encodin
40	258.8	19.3	1570	22	AAH79025 Human serine/threo
41	258.8	19.3	1570	22	AAAG9264 DNA encoding a hum
42	258.6	19.3	2367	21	AAAC61592 Human low adenosin
43	258.6	19.3	2574	21	AAF21406 Human adenosine re
44	258.6	19.3	2574	21	AAAS5284 Human cDNA differe
45	258.6	19.3	2574	24	ABK84515

ALIGNMENTS

RESULT 1
AAV23833
ID AAV23833 standard; cDNA; 2311 BP.
XX
XX
AC AAV23833;
XX
XX
DT 31-JUL-1998 (first entry)
XX
DE Human protein kinase HPK-3 coding sequence.
XX
XX
KW Protein kinase; human; HPK; signalling cascade; kinase expression;
KW Alzheimer's disease; cancer; anti-inflammatory agent; immunosuppressor;
KW asthma; multiple sclerosis; rheumatoid arthritis; lymphocytic leukaemia;
KW lymphoma; therapy; ss.
XX
XX
OS Homo sapiens.
XX
XX
PH Key Location/Qualifiers
FT CDS 379..1080
FT /tag= a

WO9811234-A2.
XX
PD 19-MAR-1998.
XX
PF 10-SEP-1997; 97WO-US15923.
XX
PR 12-SEP-1996; 96US-0712709.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Au-Young J, Guegler KJ, Hawkins PR;

PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and
 PT treating immune-related diseases and disorders, cardiovascular disease,
 PT neurodegenerative diseases and/or cancers -
 XX
 PS Disclosure; Fig 2; 310pp; English.

CC The present sequence encodes a novel protein kinase. The nucleic acids
 CC and the protein kinases they encode may be used in the treatment and
 CC diagnosis of diseases associated with inappropriate kinase expression
 CC such as immune-related diseases and disorders, cardiovascular disease,
 CC neurodegenerative diseases and/or cancers. The nucleic acids and
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays. The kinase polypeptides may be used as antigens in the production
 CC of antibodies of kinase expression and activity. Anti-kinase antibodies
 CC and kinase antagonists may also be used to down regulate kinase
 CC expression and activity. Diseases related to kinase expression and
 CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
 CC disorders, complications of organ transplantation, myocardial infarction,
 CC immune disorders, cardiomyopathies, strokes, renal failure,
 CC oxidative-stress related disorders, chronic inflammatory bowel disease,
 CC chronic inflammatory pelvic disease, multiple sclerosis, asthma,
 CC osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and
 CC reproductive disorders.

XX Sequence 1296 BP; 345 A; 333 C; 293 G; 325 T; 0 other;

Query Match 91.0%; Score 1218.2; DB 22; Length 1296;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	116	TGCTTTTCATGAAGCAGAGAGAGATGGTCTGAACGACTTTATTCAGAGATTGCCAATA	175
DB	74	TGCTTTTCATGAAGCAGAGAGAGATGGTCTGAACGACTTTATTCAGAGATTGCCAATA	133
QY	176	ACTCCTATGATCATCAACACCCCTGAAGTTCAGTCCATCTTGAAGATCTCCCACTCAGG	235
DB	134	ACTCCTATGATCATCAACACCCCTGAAGTTCAGTCCATCTTGAAGATCTCCCACTCAGG	193
QY	236	AGCCTGAGCTTTATGAATGCCAACCCCTTCTCTCCACCAAGTCTCTTCAGCAATCAACC	295
DB	194	AGCCTGAGCTTTATGAATGCCAACCCCTTCTCTCCACCAAGTCTCTTCAGCAATCAACC	253
QY	296	TTGGCCGCTGCTCCAAATCTCATGCTTAACCATCTGACTTTTCACTTTGAAAGTGATCG	355
DB	254	TTGGCCGCTGCTCCAAATCTCATGCTTAACCATCTGACTTTTCACTTTGAAAGTGATCG	313
QY	356	GAAGGGCAGTTTGGAAAGTTCTCTACGACAGACACAGGAGAGAGTCTTCTATG	415
DB	314	GAAGGGCAGTTTGGAAAGTTCTCTACGACAGACACAGGAGAGAGTCTTCTATG	373
QY	416	CAGTCAAAAGTTTACAGAGAAAGCAATCTGAAAGAAAGAGAGAGCATATTATGT	475
DB	374	CAGTCAAAAGTTTACAGAGAAAGCAATCTGAAAGAAAGAGAGAGCATATTATGT	433
QY	476	CGAGCGGAATGTTCTGTTGAAGATGTGAAGCACCCCTTTCCTGGGGCTTCACTTCT	535
DB	434	CGAGCGGAATGTTCTGTTGAAGATGTGAAGCACCCCTTTCCTGGGGCTTCACTTCT	493
QY	536	CTTTCCAGACTGCTGACAAATTTGCTTCTCTAGACTACATTAATGTTGGAGATTGT	595
DB	494	CTTTCCAGACTGCTGACAAATTTGCTTCTCTAGACTACATTAATGTTGGAGATTGT	553
QY	596	TCTACCATCTCCAGAGGGAACGCTGCTTCTGGAACCAACCGGCTCGTTTCTATGCTGCTG	655
DB	554	TCTACCATCTCCAGAGGGAACGCTGCTTCTGGAACCAACCGGCTCGTTTCTATGCTGCTG	613
QY	656	AAATAGCCAGTCTGGGCTACCTGCATTTCATCTGAACATCGTTTATAGAGACTTAAAC	715
DB	614	AAATAGCCAGTCTGGGCTACCTGCATTTCATCTGAACATCGTTTATAGAGACTTAAAC	673
QY	716	CAGAGATATTTTGTAGATTTCAGGGACACATTTCTTACTGACTTCGGACTCTGCA	775
DB	674	CAGAGATATTTTGTAGATTTCAGGGACACATTTCTTACTGACTTCGGACTCTGCA	733

QY	776	AGGAGAACATTGAACACACACACCAATCCACCTTCTGTGGCAGCCGGAGTATCTCG	835
DB	734	AGGAGAACATTGAACACACACACCAATCCACCTTCTGTGGCAGCCGGAGTATCTCG	793
QY	836	CACCTGAGTGTCTTATAGCAGCCTTATGACAGGACTGTGAGTGGTGGCTGGGAG	895
DB	794	CACCTGAGTGTCTTATAGCAGCCTTATGACAGGACTGTGAGTGGTGGCTGGGAG	853
QY	896	CTGCTTGTATGAGATGCTGTATGGCTCGCGCTTTTATAGCCGAAACACAGCTGAAA	955
DB	854	CTGCTTGTATGAGATGCTGTATGGCTCGCGCTTTTATAGCCGAAACACAGCTGAAA	913
QY	956	TGTACGACAACTTCTGAACAGCCTCTCAGCTGAAACCAATATTACAAATTCGCAA	1015
DB	914	TGTACGACAACTTCTGAACAGCCTCTCAGCTGAAACCAATATTACAAATTCGCAA	973
QY	1016	GACACCTCTCGAGGGCTCTTCGACAGAGACAGCAAGCGGCTCGGGCCCAAGATG	1075
DB	974	GACACCTCTCGAGGGCTCTTCGACAGAGACAGCAAGCGGCTCGGGCCCAAGATG	1033
QY	1076	ACTTCATGAGATTAAAGATGTCATGCTTCTCTCTTAATTAACCTGGGATGATCTCATTA	1135
DB	1034	ACTTCATGAGATTAAAGATGTCATGCTTCTCTCTTAATTAACCTGGGATGATCTCATTA	1093
QY	1136	ATAAGAGATTACTCCCTCTTTAACCCAAATGTGAGTGGGCCCAACGACCTACGGCACT	1195
DB	1094	ATAAGAGATTACTCCCTCTTTAACCCAAATGTGAGTGGGCCCAACGACCTACGGCACT	1153
QY	1196	TTGACCCCGAGTTTACGAGAGCCTGTCCCACTCCATTGGCAAGTCCCTTGACAGCG	1255
DB	1154	TTGACCCCGAGTTTACGAGAGCCTGTCCCACTCCATTGGCAAGTCCCTTGACAGCG	1213
QY	1256	TCTCTGTACAGCAGCGTCAAGGAGAGTCCGAGGCTTTCTTAGGCTTTCTATGCGC	1315
DB	1214	TCTCTGTACAGCAGCGTCAAGGAGAGTCCGAGGCTTTCTTAGGCTTTCTATGCGC	1273
QY	1316	CTCCACGGACTCTTTCTCTCTGA	1338
DB	1274	CTCCACGGACTCTTTCTCTCTGA	1296

RESULT 3

AAV74190	standard; DNA; 2346 BP.
ID	AAV74190 standard; DNA; 2346 BP.
XX	
AC	AAV74190;
XX	
DT	15-MAR-1999 (first entry)
XX	
DE	Human sgk DNA.
XX	
KW	Serum glucocorticoid regulated kinase; sgk; human; treatment; inhibitor;
KW	serine/chronic protein kinase family; antagonist; diabetic nephropathy;
KW	chronic renal failure; inflammation; Alzheimers disease; wound; ss.
XX	
OS	Homo sapiens.
XX	
PH	Key
FT	CDS
FT	45..1340
FT	/*tag= a
FT	/product= "sgk"
FT	/transl_except= (pos:1185..1187, aa:Asp)
XX	
PN	EP887081-A2.
XX	
PD	30-DEC-1998.
XX	
PF	27-MAY-1998; 98EP-0304189.
XX	
PR	27-JUN-1997; 97US-0051124.
XX	
PA	(SMIK) SMITHKLINE BEECHAM CORP.

XX	Kumar JM;
P1	WPI; 1999-047627/05.
XX	P-PSDB; AAW90139.
DR	Treating chronic renal failure, diabetic nephropathy and Alzheimer's disease - by administration of nucleic acids and antagonists which inhibit activity or expression of human serum glucocorticoid regulated kinase (sgk), a serine/threonine protein kinase
PT	
PT	
PT	
XX	Disclosure; Page 14-15; 17pp; English.
PS	
XX	This sequence encodes a novel human serum glucocorticoid regulated kinase (sgk) protein which is a member of the serine/threonine protein kinase family. This protein is used for the treatment of a subject having need to inhibit/antagonise activity or expression of human sgk polypeptide e.g. for the treatment of chronic renal failure, diabetic nephropathy, CC inflammation, Alzheimers disease and wounds.
XX	
SQ	Sequence 2346 BP; 608 A; 520 C; 518 G; 700 T; 0 other;
	Query Match 91.0%; Score 1218.2; DB 20; Length 2346;
	Best Local Similarity 99.8%; Pred. No. 0;
	Matches 1220; Conservative 0; Mismatches 3; Indels 0; Gaps 0
QY	116 TGGCTTTTCATGAACGAGCAGGAGGATGGGTCTGAACGACTTTTATTTCAGAAGATTGCCAATA 175
Db	
QY	118 TCGCTTTTCATGAACGAGCAGGAGGATGGGTCTGAACGACTTTTATTTCAGAAGATTGCCAATA 177
Db	
QY	176 ACTCTATGCATGCAAAACACCCTCGAAGTTTCAGTCCATCTTGAAAGATCTCCCAACCTCAGG 235
Db	
QY	178 ACTCTATGCATGCAAAACACCCTCGAAGTTTCAGTCCATCTTGAAAGATCTCCCAACCTCAGG 237
Db	
QY	236 AGCCTGAGCTTATGAATGCCAACCCCTTCCTCCACCAAGTCCTTCTCAGCAAAATCAACC 295
Db	
QY	238 AGCCTGAGCTTATGAATGCCAACCCCTTCCTCCACCAAGTCCTTCTCAGCAAAATCAACC 297
Db	
QY	296 TTGGCCCGTGTGCCAATCCTCATGCTAAACCATCTGACTTTCACCTCTTTGAAAGTGATCG 355
Db	
QY	298 TTGGCCCGTGTGCCAATCCTCATGCTAAACCATCTGACTTTCACCTCTTTGAAAGTGATCG 357
Db	
QY	356 GAAAGGCGCAGTTTTTGGAAAGGTTCTTCTTAGCAAGACACAAGCGCAGAGAAGTGTTCTATG 415
Db	
QY	358 GAAAGGCGCAGTTTTTGGAAAGGTTCTTCTTAGCAAGACACAAGCGCAGAGAAGTGTTCTATG 417
Db	
QY	416 CAGTCAAAGTTTTCAGAGAAAGCAATCCTGTAAGAAAAGAAAGAGAGAGCAATATTATGT 475
Db	
QY	418 CAGTCAAAGTTTTCAGAGAAAGCAATCCTGTAAGAAAAGAAAGAGAGAGCAATATTATGT 477
Db	
QY	476 CGGAGCGGAATGTTCTGTTGAAGAAATGTGAAGCACCCCTTCTCGTGGGCCCTTCACTTCT 535
Db	
QY	478 CGGAGCGGAATGTTCTGTTGAAGAAATGTGAAGCACCCCTTCTCGTGGGCCCTTCACTTCT 537
Db	
QY	536 CTTTCCAGACTGCTGACAAATTTGTAATTTGTCTTAGACTACATAATCGTGAGAGTTGT 595
Db	
QY	538 CTTTCCAGACTGCTGACAAATTTGTAATTTGTCTTAGACTACATAATCGTGAGAGTTGT 597
Db	
QY	596 TCTACCATCTCCAGAGGAAACGCTGCTTCTTGAAACCAACGGGCTCGTTTCTATGCTGCTG 655
Db	
QY	598 TCTACCATCTCCAGAGGAAACGCTGCTTCTTGAAACCAACGGGCTCGTTTCTATGCTGCTG 657
Db	
QY	656 AAATAGCCAGTGCCCTTGGGCTACCTGCATTCACCTGAACATCGTTTATAGAGACTTAAAC 715
Db	
QY	658 AAATAGCCAGTGCCCTTGGGCTACCTGCATTCACCTGAACATCGTTTATAGAGACTTAAAC 717
Db	
QY	716 CAGAGAATATTTTGTAGATTTCAGAGGACACATTGTCTTACTGACTTCGGACTCTGCA 775
Db	
QY	718 CAGAGAATATTTTGTAGATTTCAGAGGACACATTGTCTTACTGACTTCGGACTCTGCA 777
Db	
QY	776 AGGAGAACTTGAACACAAAGCAACAATCCACTTCTGTGGCACCGCGGAGTATCTCG 835
Db	
QY	778 AGGAGAACTTGAACACAAAGCAACAATCCACTTCTGTGGCACCGCGGAGTATCTCG 837
Db	

PT New nucleic acid encoding cell-volume regulating kinase h-egk and
 PT related proteins - used for diagnosis and treatment of diseases
 PT involving changes in cell volume, e.g. renal insufficiency,
 PT inflammation, infections etc.
 XX Disclosure; Fig 1; 15pp; German.

PS
 CC The human cell-volume regulating kinase h-egk is inhibited by the
 CC swelling of cells (or presence of urea), whereas cell shrinkage
 CC stimulates its expression. The nucleic acid h-egk, and fragments, are
 CC particularly used to detect changes in cell volume, specifically for
 CC diagnosis of conditions that involve such changes, e.g. hyper- and hypo-
 CC natriemia, diabetes mellitus, renal insufficiency, hypercatabolism,
 CC hepatic encephalopathy, inflammation, microbial/viral infection, fructose
 CC intolerance, hyper- and hypo-glycaemia and Alzheimer's disease.
 CC The nucleic acid, protein and products including receptors that bind
 CC h-egk, can be used to treat these disorders.

XX
 SQ Sequence 2370 BP; 636 A; 517 C; 513 G; 704 T; 0 other;
 Query Match 91.0%; Score 1218.2; DB 19; Length 2370;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	116	TGGCTTTCATGACGAGGAGGATGGTCTGAACGACTTTATTCAGAGATTGCCAATA	175
Db	116	TGCGTTTTCATGACGAGGAGGATGGTCTGAACGACTTTATTCAGAGATTGCCAATA	175
Qy	176	ACTCCTATGATGCAACACCCCTGAAGTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG	235
Db	176	ACTCCTATGATGCAACACCCCTGAAGTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG	235
Qy	236	AGCCTGAGCTTATGAATGCCAACCCCTTCTCTCCACCAAGTCTCTTCAGCAAAATCAACC	295
Db	236	AGCCTGAGCTTATGAATGCCAACCCCTTCTCTCCACCAAGTCTCTTCAGCAAAATCAACC	295
Qy	296	TTGGCCCGTCGTCGAATCTCATGCTAAACATCTGACTTTTCACTTTTCACTTTTCACT	355
Db	296	TTGGCCCGTCGTCGAATCTCATGCTAAACATCTGACTTTTCACTTTTCACTTTTCACT	355
Qy	356	GAAAGGCGAGTTTGGAAAGGTTCTTCTAGCAAGACCAAGGCAAGAGAGTGTCTTATG	415
Db	356	GAAAGGCGAGTTTGGAAAGGTTCTTCTAGCAAGACCAAGGCAAGAGAGTGTCTTATG	415
Qy	416	CAGTCAAAATTTTACAGAAAGCAATCTGTAAGAAAGAGGAGAAATATATGT	475
Db	416	CAGTCAAAATTTTACAGAAAGCAATCTGTAAGAAAGAGGAGAAATATATGT	475
Qy	476	CGGAGCGGAATGTTCTTGAAGAAATGTGAAGACCCCTTTCTGTTGGGCTTCACTTCT	535
Db	476	CGGAGCGGAATGTTCTTGAAGAAATGTGAAGACCCCTTTCTGTTGGGCTTCACTTCT	535
Qy	536	CTTTCCAGACTGCTGACAAATTTGACTTTCTCTAGACTACATTAATGTTGGAGAGTTGT	595
Db	536	CTTTCCAGACTGCTGACAAATTTGACTTTCTCTAGACTACATTAATGTTGGAGAGTTGT	595
Qy	596	TCTACCATCTCCAGAGGGAACGCTGCTTCTGGAACCAACGAGCTGCTTTCTATGCTGCTG	655
Db	596	TCTACCATCTCCAGAGGGAACGCTGCTTCTGGAACCAACGAGCTGCTTTCTATGCTGCTG	655
Qy	656	AAATAGCCAGTGGCTTGGGCTACCTGCAATTCAGTGAACATCGTTTATAGAGACTTAAAC	715
Db	656	AAATAGCCAGTGGCTTGGGCTACCTGCAATTCAGTGAACATCGTTTATAGAGACTTAAAC	715
Qy	716	CAGAGAAATTTTGTAGATTCAGAGGACACATTTGCTTACTGATTTTCGGACTCTGCA	775
Db	716	CAGAGAAATTTTGTAGATTCAGAGGACACATTTGCTTACTGATTTTCGGACTCTGCA	775
Qy	776	AGGAGAAATTCAGAGGACACATTCACCTTCTGTTGGCAGCCGAGTATCTCG	835
Db	776	AGGAGAAATTCAGAGGACACATTCACCTTCTGTTGGCAGCCGAGTATCTCG	835
Qy	836	CACCTGAGGTGCTTTCATAGCAGCCTTATGACAGGACTGTGGACTGTGCTGGGAG	895

Db	836	CACCTGAGGTGCTTTCATAGCAGCCTTATGACAGGACTGTGGACTGTGCTGGGAG	895
Qy	896	CTGCTCTTGTATGAGATGCTGTATGGCTGCGGCTTTTATAGCCGAAACACAGCTGAAA	955
Db	896	CTGCTCTTGTATGAGATGCTGTATGGCTGCGGCTTTTATAGCCGAAACACAGCTGAAA	955
Qy	956	TGTACGACAAATTTCTGAACAAGCCCTCTCCAGCTGAAACCAAAATATTTACAAATTTCCGCAA	1015
Db	956	TGTACGACAAATTTCTGAACAAGCCCTCTCCAGCTGAAACCAAAATATTTACAAATTTCCGCAA	1015
Qy	1016	GACACCTCTGAGGAGGCTCTCTCAGAGGACAGGACAAAGCCGCTCGGGGCCAAGGATG	1075
Db	1016	GACACCTCTCTGAGGAGGCTCTCTCAGAGGACAGGACAAAGCCGCTCGGGGCCAAGGATG	1075
Qy	1076	ACTTCAATGAGATTAAGAGTCATGCTTCTTCTCTTAAATTAATGAGGATGCTCTATTA	1135
Db	1076	ACTTCAATGAGATTAAGAGTCATGCTTCTTCTCTTAAATTAATGAGGATGCTCTATTA	1135
Qy	1136	ATAAGAGATTAATCTCCCTCTTTTAAACCAAAATGTAGTGGGCCCAACGACTACGGCACT	1195
Db	1136	ATAAGAGATTAATCTCCCTCTTTTAAACCAAAATGTAGTGGGCCCAACGACTACGGCACT	1195
Qy	1196	TTGACCCCGAGTTTACCGAAGAGCCTGTCCCAACTCCATTTGGCAAGTCCCTTGAACGCG	1255
Db	1196	TTGACCCCGAGTTTACCGAAGAGCCTGTCCCAACTCCATTTGGCAAGTCCCTTGAACGCG	1255
Qy	1256	TCCTGCTGACAGCCAGGCTCAAGGAAGCTGCGGAGGCTTTCCTAGGCTTTTCTATGCGC	1315
Db	1256	TCCTGCTGACAGCCAGGCTCAAGGAAGCTGCGGAGGCTTTCCTAGGCTTTTCTATGCGC	1315
Qy	1316	CTCCACGAGCTCTTTCTCTCTGA	1338
Db	1316	CTCCACGAGCTCTTTCTCTCTGA	1338

RESULT 5

ABK84749

ID ABK84749 standard; cDNA; 2370 BP.

XX AC ABK84749;

XX AC ABK84749;

DT 14-AUG-2002 (first entry)

XX Human cDNA differentially expressed in granulocytic cells #1320.

Human; ss; granulocytic cell; DNA chip; bacterial infection;
 viral infection; parasitic infection; protozoal infection;
 fungal infection; sterile inflammatory disease; psoriasis;
 rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
 cardiac reperfusion injury; renal reperfusion injury; ARDS;
 adult respiratory distress syndrome; inflammatory bowel disease;
 Crohn's disease; ulcerative colitis; periodontal disease;
 granulocyte activation; chronic inflammation; allergy.

XX Homo sapiens.

XX WO200228999-A2.

XX 11-APR-2002.

XX 03-OCT-2001; 2001WO-US30821.

XX 03-OCT-2000; 2000US-237189P.

XX (GENE-) GENE LOGIC INC.

XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

XX WPI; 2002-435328/46.

PT Detecting granulocyte activation by detecting differential expression
 of genes associated with granulocyte activation, which serves as

diagnostic markers that is useful for monitoring disease states and drug toxicity

Claim 1; SEQ ID No 1320; 114pp; English.

The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease, also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection, and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Query March 91.08; Score 1218.2; DB 24; Length 2370; Best Local Similarity 99.8%; Pred. No. 0; Matches 1220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

116 TGGCTTTTCATGAAGCAGAGGAGGATGGTCTGAACGACTTTATTTCAGAAAGATTGCCAATA 175
116 TCGCTTTTCATGAAGCAGAGGAGGATGGTCTGAACGACTTTATTTCAGAAAGATTGCCAATA 175
176 ACTCTATGATGCAACACCTGAAGTTTCTGAGTCCATTTGAGAGATCTCCCAACCTCAGG 235
176 ACTCTATGATGCAACACCTGAAGTTTCTGAGTCCATTTGAGAGATCTCCCAACCTCAGG 235
236 AGCTGAGCTTATGATGCAACACCTTCTCTCCACCAAGTCTTCTCAGCAATCAACC 295
236 AGCTGAGCTTATGATGCAACACCTTCTCTCCACCAAGTCTTCTCAGCAATCAACC 295
296 TTGGCCCGCTCGTCCAACTCTCATGCTAAACCATCTGACTTTTCACTTTTGAAGTATCG 355
296 TTGGCCCGCTCGTCCAACTCTCATGCTAAACCATCTGACTTTTCACTTTTGAAGTATCG 355
356 GAAAGGCGAGTTTGGAAAGGTTCTTCTAGCAAGACACAAAGGAGAGAGTGTCTATG 415
356 GAAAGGCGAGTTTGGAAAGGTTCTTCTAGCAAGACACAAAGGAGAGAGTGTCTATG 415
416 CAGTCAAAAGTTTACAGAAAGAGCAATCTGTAAGAGAGAGAGAGCAATATATGT 475
416 CAGTCAAAAGTTTACAGAAAGAGCAATCTGTAAGAGAGAGAGAGCAATATATGT 475
476 CGGAGCGGAATGTTCTGTTGAAGAAATGTGAAGCACCCTTTCTCTGGTGGGCTTCACTTCT 535

476 CGGAGCGGAATGTTCTGTTGAAGAAATGTGAAGCACCCTTTCTCTGGTGGGCTTCACTTCT 535
536 CTTTCCAGACTGCTGACAAATTTGTACTTTGTCTAGACTACATTAAATGGTGGAGATTGT 595
536 CTTTCCAGACTGCTGACAAATTTGTACTTTGTCTAGACTACATTAAATGGTGGAGATTGT 595
596 TCTACCATCTCCAGAGGGAACGCTGCTTCTGGAACCAAGGCTCGTTCTATGCTGCTG 655
596 TCTACCATCTCCAGAGGGAACGCTGCTTCTGGAACCAAGGCTCGTTCTATGCTGCTG 655
656 AAATAGCCAGTGCCTTGGGCTACCTGCAATTCACCTGAACATCGTTTATAGAGACTTAAAC 715
656 AAATAGCCAGTGCCTTGGGCTACCTGCAATTCACCTGAACATCGTTTATAGAGACTTAAAC 715
716 CAGAGAAATATTTGCTAGATTTACAGGGGACACATTTGCTTACTGACTTCGGACTCTGCA 775
716 CAGAGAAATATTTGCTAGATTTACAGGGGACACATTTGCTTACTGACTTCGGACTCTGCA 775
776 AGGAGAAATTTGAACACACAGCAACATCCACCTTCTGTGCGACCGCGAGTATCTCG 835
776 AGGAGAAATTTGAACACACAGCAACATCCACCTTCTGTGCGACCGCGAGTATCTCG 835
836 CACCTGAGTGTCTTCAATAGCAGCCTTATGACAGGACTGTGAGTGGTGGCTGGGAG 895
836 CACCTGAGTGTCTTCAATAGCAGCCTTATGACAGGACTGTGAGTGGTGGCTGGGAG 895
896 CTGTCTTGTATGAGTGTGATGGCTCGCGCTTTTATAGCCGAAACACAGCTGAAA 955
896 CTGTCTTGTATGAGTGTGATGGCTCGCGCTTTTATAGCCGAAACACAGCTGAAA 955
956 TGTACGACAACTTCTGACAAAGCCTTCCAGCTGAACCAAAATATTACAAATTCGCA 1015
956 TGTACGACAACTTCTGACAAAGCCTTCCAGCTGAACCAAAATATTACAAATTCGCA 1015
1016 GACACCTCTGGAGGCTCTCTGACAGAGCAGGACAAAGGCGCTCGGGGCAAGGATG 1075
1016 GACACCTCTGGAGGCTCTCTGACAGAGCAGGACAAAGGCGCTCGGGGCAAGGATG 1075
1076 ACTTATGAGATTAAGAGTATGTTCTTCTTCTTAAATTAATCGGAGTATCTCATTA 1135
1076 ACTTATGAGATTAAGAGTATGTTCTTCTTCTTAAATTAATCGGAGTATCTCATTA 1135
1136 ATAAGAAATTAATCTCCCTCTTTTAAACCAATGTAGTGGGCGCCCAAGCTACGCACT 1195
1136 ATAAGAAATTAATCTCCCTCTTTTAAACCAATGTAGTGGGCGCCCAAGCTACGCACT 1195
1196 TTGACCCCGAGTTTACCGAAGAGCCTGTCCCAACTCCATTGGCAAGTCCCTTGACAGCG 1255
1196 TTGACCCCGAGTTTACCGAAGAGCCTGTCCCAACTCCATTGGCAAGTCCCTTGACAGCG 1255
1256 TCTTGTGTCAGCAGCGCTCAAGGAGCTGCGAGGCTTTCTAGGCTTTTCTATGCGC 1315
1256 TCTTGTGTCAGCAGCGCTCAAGGAGCTGCGAGGCTTTCTAGGCTTTTCTATGCGC 1315
1316 CTCGCCAGGACTTTTCTCTCTGA 1338
1316 CTCGCCAGGACTTTTCTCTCTGA 1338

RESULT 6

ABN97360

ID ABN97360 standard; DNA; 2370 BP.

XX

AC ABN97360;

XX

DT 13-AUG-2002 (first entry)

XX

DE Gene #3858 used to diagnose liver cancer.

XX

KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.

XX OS Homo sapiens.
XX PN WO200229103-A2.
XX PD 11-APR-2002.
XX PF 02-OCT-2001; 2001WO-US30589.
XX PR 02-OCT-2000; 2000US-237054P.
XX PA (GENE-) GENE LOGIC INC.
XX PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
XX DR WPI; 2002-426119/45.
XX PT Diagnosing and detecting the progression of liver cancer,
XX PT hepatocellular carcinoma or metastatic liver tumor in a patient,
XX PT involves detecting the level of expression of two or more genes in a
XX PT liver tissue sample
XX PS Claim 1; SEQ ID NO 3858; 298pp; English.
XX CC The invention relates to a novel method for diagnosing and detecting the
XX CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
XX CC tumor in a patient, and differentiating metastatic liver cancer from
XX CC hepatocellular carcinoma in a patient, involving detecting the level of
XX CC expression of two or more genes represented in ABN93503-ABN97455 in a
XX CC tissue sample. The method of the invention has hepatotropic, and
XX CC cytostatic activity. The method is useful for diagnosing and detecting
XX CC the progression of liver cancer, hepatocellular carcinoma and metastatic
XX CC liver carcinoma in a patient. The method is useful for identifying
XX CC expression profiles which serve as useful diagnostic markers as well as
XX CC markers that can be used to monitor disease states, disease progression,
XX CC drug toxicity, drug efficacy and drug metabolism.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 2370 BP; 636 A; 517 C; 513 G; 704 T; 0 other;

Query Match 91.0%; Score 1218.2; DB 24; Length 2370;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 116 TGGCTTTCATGACGACGAGGAGTGGTCTGAACGACTTTATTCAGAGATTGCCAATA 175
DB 116 TCGCTTTTCATGAAGCAGAGAGGAGTGGTCTGAACGACTTTATTCAGAGATTGCCAATA 175
QY 176 ACTCCTATGATGCAACACCCCTGAAGTTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG 235
DB 176 ACTCCTATGATGCAACACCCCTGAAGTTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG 235
QY 236 AGCCTGAGCTTATGAATGCCAACCCCTTCTCCTCCACCAAGTCTTCTCAGCAAAATCAACC 295
DB 236 AGCCTGAGCTTATGAATGCCAACCCCTTCTCCTCCACCAAGTCTTCTCAGCAAAATCAACC 295
QY 296 TTGGCCCGCTCGTCCATCCTCATGCTTAACCATCTGACTTTTCACTTCTTGAAGTATCG 355
DB 296 TTGGCCCGCTCGTCCATCCTCATGCTTAACCATCTGACTTTTCACTTCTTGAAGTATCG 355
QY 356 GAAAGGGCAGCTTTTGGAAAGGTTCTTCTAGCAAGACACAAGGCGAGAGAGTGTCTTATG 415
DB 356 GAAAGGGCAGCTTTTGGAAAGGTTCTTCTAGCAAGACACAAGGCGAGAGAGTGTCTTATG 415
QY 416 CAGTCAAAGTTTACAGAAGAAAGCAATCCTGAAAGAAAGAGGAGCAATATTATGT 475
DB 416 CAGTCAAAGTTTACAGAAGAAAGCAATCCTGAAAGAAAGAGGAGCAATATTATGT 475
QY 476 CGAGGCGGAATGTTCTGTTGAAGAAATGTGAAGACCCCTTCTCGTGGGGCTTCACTTCT 535
DB 476 CGAGGCGGAATGTTCTGTTGAAGAAATGTGAAGACCCCTTCTCGTGGGGCTTCACTTCT 535

QY 536 CTTTCCAGACTGCTGACAAATTTGTACTTTGTCTAGACTACATTAAATGTTGGAGAGTTGT 595
DB 536 CTTTCCAGACTGCTGACAAATTTGTACTTTGTCTAGACTACATTAAATGTTGGAGAGTTGT 595
QY 596 TCTACCATCTCCAGAGGGAACGCTGCTTCTGGMACCGGGCTCGTTTCTATGCTGCTG 655
DB 596 TCTACCATCTCCAGAGGGAACGCTGCTTCTGGMACCGGGCTCGTTTCTATGCTGCTG 655
QY 656 AAATAGCCAGTGCCTTGGGCTACCTGCATTCACTGAACATCGTTTATAGAGACTTAAAC 715
DB 656 AAATAGCCAGTGCCTTGGGCTACCTGCATTCACTGAACATCGTTTATAGAGACTTAAAC 715
QY 716 CAGAGAATATTTTGTGTAGATTACAGGGACACATTGCTTCTACTGACTTCGGACTCTGCA 775
DB 716 CAGAGAATATTTTGTGTAGATTACAGGGACACATTGCTTCTACTGACTTCGGACTCTGCA 775
QY 776 AGGAGAACATTGAACACACAGACACACATCCACCTTCTGTGGCAGCCGGAGTATCTCG 835
DB 776 AGGAGAACATTGAACACACAGACACACATCCACCTTCTGTGGCAGCCGGAGTATCTCG 835
QY 836 CACCTGAGTGTCTTCAATAGCAGCCTTATGACAGGACTGTGACTGCTGCTGGGAG 895
DB 836 CACCTGAGTGTCTTCAATAGCAGCCTTATGACAGGACTGTGACTGCTGCTGGGAG 895
QY 896 CTGCTTGTATGAGATGCTGTATGGCTGCGCTTTTATAGCCGAAACACAGCTGAAA 955
DB 896 CTGCTTGTATGAGATGCTGTATGGCTGCGCTTTTATAGCCGAAACACAGCTGAAA 955
QY 956 TGTACGACAAACATTCTGAACAAAGCCTTCCAGCTGAACCAATATTACAAATTCGCA 1015
DB 956 TGTACGACAAACATTCTGAACAAAGCCTTCCAGCTGAACCAATATTACAAATTCGCA 1015
QY 1016 GACACCTCTGGAGGCGCTCTGCAAGGACAGGACAAAGCGCTCGGGCCCAAGATG 1075
DB 1016 GACACCTCTGGAGGCGCTCTGCAAGGACAGGACAAAGCGCTCGGGCCCAAGATG 1075
QY 1076 ACTTCAATGAGATTAAGAGTCAATGCTTCTTCTTAAATTAACCTGGGATGATCTCATTA 1135
DB 1076 ACTTCAATGAGATTAAGAGTCAATGCTTCTTCTTAAATTAACCTGGGATGATCTCATTA 1135
QY 1136 ATAAGAGATTAATCTCCCTTTTAAACCAATGTAGTGGGCGCCCAACGACTACGGCACT 1195
DB 1136 ATAAGAGATTAATCTCCCTTTTAAACCAATGTAGTGGGCGCCCAACGACTACGGCACT 1195
QY 1196 TTGACCCCGAGTTTACCGAAGAGCCTGTCCCAACTCCATTTGGCAAGTCCCTTGACAGCG 1255
DB 1196 TTGACCCCGAGTTTACCGAAGAGCCTGTCCCAACTCCATTTGGCAAGTCCCTTGACAGCG 1255
QY 1256 TCTCTGTCACAGCCAGCTCAAGAGAGTCCGAGGCTTTCTTAGGCTTTTCTATGCGC 1315
DB 1256 TCTCTGTCACAGCCAGCTCAAGAGAGTCCGAGGCTTTCTTAGGCTTTTCTATGCGC 1315
QY 1316 CTCCACGAGACTTTTCTCTCTGA 1338
DB 1316 CTCCACGAGACTTTTCTCTCTGA 1338

RESULT 7
ABL70006
ID ABL70006 standard; DNA; 2370 BP.
XX
XX ABL70006;
XX AC
XX AC
XX DT 15-MAY-2002 (first entry)
XX
XX Pancreas cancer related gene sequence SEQ ID NO:8343.
XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
XX stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
XX cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
XX gene; ds.
XX

OS Homo sapiens.

XX WO200194629-A2.

XX 13-DEC-2001.

PD 30-MAY-2001; 2001WO-US10838.

XX 05-JUN-2000; 2000US-209473P.

PR 05-JUN-2000; 2000US-209531P.

PR 18-SEP-2000; 2000US-233133P.

PR 18-SEP-2000; 2000US-233617P.

PR 20-SEP-2000; 2000US-234009P.

PR 20-SEP-2000; 2000US-234034P.

PR 20-SEP-2000; 2000US-234052P.

PR 22-SEP-2000; 2000US-234509P.

PR 22-SEP-2000; 2000US-234567P.

PR 25-SEP-2000; 2000US-234923P.

PR 25-SEP-2000; 2000US-234924P.

PR 25-SEP-2000; 2000US-235077P.

PR 25-SEP-2000; 2000US-235082P.

PR 25-SEP-2000; 2000US-235134P.

PR 25-SEP-2000; 2000US-235280P.

PR 26-SEP-2000; 2000US-235637P.

PR 26-SEP-2000; 2000US-235638P.

PR 27-SEP-2000; 2000US-235711P.

PR 27-SEP-2000; 2000US-235720P.

PR 27-SEP-2000; 2000US-235720P.

PR 27-SEP-2000; 2000US-235840P.

PR 27-SEP-2000; 2000US-235863P.

PR 28-SEP-2000; 2000US-236028P.

PR 28-SEP-2000; 2000US-236032P.

PR 28-SEP-2000; 2000US-236033P.

PR 28-SEP-2000; 2000US-236034P.

PR 28-SEP-2000; 2000US-236109P.

PR 28-SEP-2000; 2000US-236111P.

PR 29-SEP-2000; 2000US-236842P.

PR 29-SEP-2000; 2000US-236891P.

PR 02-OCT-2000; 2000US-237172P.

PR 02-OCT-2000; 2000US-237173P.

PR 02-OCT-2000; 2000US-237278P.

PR 02-OCT-2000; 2000US-237294P.

PR 02-OCT-2000; 2000US-237295P.

PR 03-OCT-2000; 2000US-237316P.

PR 03-OCT-2000; 2000US-237425P.

PR 03-OCT-2000; 2000US-237598P.

PR 03-OCT-2000; 2000US-237604P.

PR 03-OCT-2000; 2000US-237606P.

PR 03-OCT-2000; 2000US-237608P.

PR 01-NOV-2000; 2000US-244867P.

PR 01-NOV-2000; 2000US-245084P.

XX (AVAL-) AVALON PHARM.

XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;

PI Soppet DR, Weaver Z;

XX WPI; 2002-188264/24.

XX Screening for anti-neoplastic agent involves exposing cells to a

PT chemical agent to be tested for anti-neoplastic activity, and

PT determining a change in expression of a gene of a signature gene set

XX Claim 1; SEQ ID 8343; 44pp; English.

XX The present invention describes a method (M1) for screening for an

CC anti-neoplastic agent. The method involves exposing cells to a chemical

CC agent to be tested for anti-neoplastic activity, determining a change in

CC expression of at least one gene (I) of a signature gene set, where (I)

CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664

CC to ABL70110), or is at least 95% identical to (S), where a change in

CC expression is indicative of anti-neoplastic activity. (I) has cytostatic

CC activity and can be used in gene therapy. M1 can be used for screening

CC an anti-neoplastic agent, and can be used for producing a product which

CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilms' tumour.

XX Sequence 2370 BP; 636 A; 517 C; 513 G; 704 T; 0 other;

Query Match 91.0%; Score 1218.2; DB 24; Length 2370;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 116 TGGCTTTTCAATGAAGCAGAGGAGGATGGTCTCAACGACTTTATTCAGAGATTGCCAATA 175

DB 116 TGGCTTTTCAATGAAGCAGAGGAGGATGGTCTCAACGACTTTATTCAGAGATTGCCAATA 175

QY 176 ACTCTCTATGCTGCAACACACCTGGAAGTTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG 235

DB 176 ACTCTCTATGCTGCAACACACCTGGAAGTTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG 235

QY 236 AGCTTGAGCTTATGAATGCCAACCTTCTCTCCCAAGTCTCTTCAGCAAAATCAACC 295

DB 236 AGCTTGAGCTTATGAATGCCAACCTTCTCTCCCAAGTCTCTTCAGCAAAATCAACC 295

QY 296 TTGGCCCGTCTGCTCAATCTCATGTAACCATCTGACTTTTCTTCTTGAAGTATCG 355

DB 296 TTGGCCCGTCTGCTCAATCTCATGTAACCATCTGACTTTTCTTCTTGAAGTATCG 355

QY 356 GAAAGGGCAGTTTGGGAAAGTTTCTTAGCAAGACACAAAGGAGAGAGTGTCTTATG 415

DB 356 GAAAGGGCAGTTTGGGAAAGTTTCTTAGCAAGACACAAAGGAGAGAGTGTCTTATG 415

QY 416 CAGTCAAAGTTTACAGAAAGAAAGCAATCTGAAAGAAAGAGAGAGATATATGT 475

DB 416 CAGTCAAAGTTTACAGAAAGAAAGCAATCTGAAAGAAAGAGAGAGATATATGT 475

QY 476 CGGAGCGGAATGTTCTGTTGAAGATGTGAAGCACCCTTCTCTGGTGGGCTTCACTTCT 535

DB 476 CGGAGCGGAATGTTCTGTTGAAGATGTGAAGCACCCTTCTCTGGTGGGCTTCACTTCT 535

QY 536 CTTTCCAGACTGCTGACAAATGTACTTTGTCTAGACTACATTAATGTTGGAGAGTGT 595

DB 536 CTTTCCAGACTGCTGACAAATGTACTTTGTCTAGACTACATTAATGTTGGAGAGTGT 595

QY 596 TCTACCATCTCCAGAGGGAACGCTGCTTCTGGAACACCGGGCTCTTTCTATGCTGCTG 655

DB 596 TCTACCATCTCCAGAGGGAACGCTGCTTCTGGAACACCGGGCTCTTTCTATGCTGCTG 655

QY 656 AATAGCCAGTCTGGGCTACCTGCTGATGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGG 715

DB 656 AATAGCCAGTCTGGGCTACCTGCTGATGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGG 715

QY 716 CAGAGAAATTTTGTCTAGATTTCACAGGACACATCTCTTACTGACTTCGGACTCTGCA 775

DB 716 CAGAGAAATTTTGTCTAGATTTCACAGGACACATCTCTTACTGACTTCGGACTCTGCA 775

QY 776 AGGAGAAATTTGAAACAAACAGCACAACATCCACCTTCTGTTGGCAGCCGGAGTATCTCG 835

DB 776 AGGAGAAATTTGAAACAAACAGCACAACATCCACCTTCTGTTGGCAGCCGGAGTATCTCG 835

QY 836 CACCTGAGTGTCTTATAGCAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGG 895

DB 836 CACCTGAGTGTCTTATAGCAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGG 895

QY 896 CTGCTTTGATGAGTGTGATGGCTGCTGGCTGCTTTTATAGCCGAAACACAGCTGAAA 955

DB 896 CTGCTTTGATGAGTGTGATGGCTGCTGGCTGCTTTTATAGCCGAAACACAGCTGAAA 955

QY 956 TGTACGACAACTTCTGAAACAGGCTCTCCAGCTGAAACCAATATATACAAATTCGCAA 1015

DB 956 TGTACGACAACTTCTGAAACAGGCTCTCCAGCTGAAACCAATATATACAAATTCGCAA 1015

Db 956 TGTACGACAACTTCTGACACAGCCTCTCAGCTGAAACCAATATTACAAAATTCGCCAA 1015
 Qy 1016 GACACCTCTCGAGGGCTCTCTGAGAGGACAGACAAAGCGCTCGGGCCCAAGGATG 1075
 Db 1016 GACACCTCTCGAGGGCTCTCTGAGAGGACAGACAAAGCGCTCGGGCCCAAGGATG 1075
 Qy 1076 ACTTCATGGAGATTAAAGATCATGTCTTCTCTCTTAATTAAGTGGATGATCTCATTA 1135
 Db 1076 ACTTCATGGAGATTAAAGATCATGTCTTCTCTCTTAATTAAGTGGATGATCTCATTA 1135
 Qy 1136 ATAAGAAGATTACTCCCGCTTTAAACCAAAATGTAGTGGGCCCAAGCACTAGGCAC 1195
 Db 1136 ATAAGAAGATTACTCCCGCTTTAAACCAAAATGTAGTGGGCCCAAGCACTAGGCAC 1195
 Qy 1196 TTGACCCCGAGTTTACCGAAGAGCTGTCCCCAACTCCATTGGCAAGTCCCTGACAGG 1255
 Db 1196 TTGACCCCGAGTTTACCGAAGAGCTGTCCCCAACTCCATTGGCAAGTCCCTGACAGG 1255
 Qy 1256 TCCTGTCACAGCCAGGCTCAAGGAAGCTGCGAGGCTTTCTTAGGCTTTTCTATGCGC 1315
 Db 1256 TCCTGTCACAGCCAGGCTCAAGGAAGCTGCGAGGCTTTCTTAGGCTTTTCTATGCGC 1315
 Qy 1316 CTCCACGGACTCTTTCTCTCTGA 1338
 Db 1316 CTCCACGGACTCTTTCTCTCTGA 1338

RESULT 8

AAZ33647
 ID AAZ33647 standard; cDNA; 2281 BP.
 AC AAZ33647;
 DT 08-DEC-1999 (first entry)
 DE Human breast tumour-associated EST 37.
 EX
 KW Expressed sequence tag; EST; human; breast; cancer; gene therapy;
 KW treatment; tumour; cytostatic; medicament; ss.
 XX
 OS Homo sapiens.
 XX
 PN DE19813839-AL.
 XX
 PD 23-SEP-1999.
 XX
 XX 20-MAR-1998; 98DE-1013839.
 PF
 XX 20-MAR-1998; 98DE-1013839.
 PR
 XX (META-) METAGEN GES GENOMFORSCHUNG MBH.
 PA
 XX Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
 XX WPI; 1999-528981/45.
 DR P-PSDB; AAY48573.
 XX
 PT Human nucleic acid sequences and protein products from tumor breast
 PT tissue, useful for breast cancer therapy -
 XX
 PS Claim 1a; 116-117; 189pp; German.
 XX
 CC This invention describes novel human nucleic acid sequences from tumor
 CC breast tissue which have cytostatic activity. The nucleic acid sequences
 CC can be used to produce and isolate full-length gene sequences. They can
 CC be used to express proteins, which can be used as tools to find an
 CC activity against breast cancer. The sequences can be used in sense or
 CC antisense form. They are especially useful for medicaments for gene
 CC therapy to treat breast cancer. AAZ33611-248617 represents expressed
 CC sequence tags described in the method of the invention.
 XX
 XX Sequence 2281 BP; 601 A; 498 C; 494 G; 688 T; 0 other;
 SQ

Query Match 85.5%; Score 1144; DB 20; Length 2281;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 195 CCCTGAAGTTCAGTCCCATCTTGAAGATCTCCCAACCTCAGGAGCCTGAGCTTATGATGC 254
 Db 95 CCCTGAAGTTCAGTCCCATCTTGAAGATCTCCCAACCTCAGGAGCCTGAGCTTATGATGC 154
 Qy 255 CAACCCCTTCTCTCCACCAAGTCTTCTCAGCAAAATCAACCTTGGCCCGCTGCTCCCAATCC 314
 Db 155 CAACCCCTTCTCTCCACCAAGTCTTCTCAGCAAAATCAACCTTGGCCCGCTGCTCCCAATCC 214
 Qy 315 TCATGTAAACCATCTGACTTTCACCTTCTTGAAGTATCGGAAAGCGCATTTTGGAAA 374
 Db 215 TCATGTAAACCATCTGACTTTCACCTTCTTGAAGTATCGGAAAGCGCATTTTGGAAA 274
 Qy 375 GGTTCCTTCTAGCAAGACACAAGGACAGAAGTGTCTATGACAGTCAAAAGTTTACAGAA 434
 Db 275 GGTTCCTTCTAGCAAGACACAAGGACAGAAGTGTCTATGCAAGTCAAAAGTTTACAGAA 334
 Qy 435 GAAAGCAATCTCTGAAAAGAAAGAGGAGAGCATATTTATGTCGGAGCGGAATGTTCTGTT 494
 Db 335 GAAAGCAATCTCTGAAAAGAAAGAGGAGAGCATATTTATGTCGGAGCGGAATGTTCTGTT 394
 Qy 495 GAAAGATGTGAAGCAACCTTTCTGTGGCCCTTCACTTCTCTTTCCAGACTGCTGACAA 554
 Db 395 GAAAGATGTGAAGCAACCTTTCTGTGGCCCTTCACTTCTCTTTCCAGACTGCTGACAA 454
 Qy 555 ATTGTACTTTGTCTAGACTACATTAATGTTGGAGAGTGTCTTACATCTCCAGAGGA 614
 Db 455 ATTGTACTTTGTCTAGACTACATTAATGTTGGAGAGTGTCTTACATCTCCAGAGGA 514
 Qy 615 ACGCTGCTTCTGGAACACCGGCTCGTTTCTATGCTGTGTAATAGACCAAGTGCCTTGGG 674
 Db 515 ACGCTGCTTCTGGAACACCGGCTCGTTTCTATGCTGTGTAATAGACCAAGTGCCTTGGG 574
 Qy 675 CTACCTGCAATCTCAAGCAATCGTTTATAGACTTTAAACCAAGAGATATTTTGTGTA 734
 Db 575 CTACCTGCAATCTCAAGCAATCGTTTATAGACTTTAAACCAAGAGATATTTTGTGTA 634
 Qy 735 TTCACAGGGACACATTTGCTTACTGACTTCGGACTCTGCAAGGAGAAATTCACACAA 794
 Db 635 TTCACAGGGACACATTTGCTTACTGACTTCGGACTCTGCAAGGAGAAATTCACACAA 694
 Qy 795 CAGCACAAATCCACCTTCTGTGGCACCGCGAGTATCTCGACCTGAGGTGCTTCATAA 854
 Db 695 CAGCACAAATCCACCTTCTGTGGCACCGCGAGTATCTCGACCTGAGGTGCTTCATAA 754
 Qy 855 GCAGCCTTATGACAGACTGTGGAAGTGGTGGCTGGGAGCTGTCTTGTATGAGATGCT 914
 Db 755 GCAGCCTTATGACAGACTGTGGAAGTGGTGGCTGGGAGCTGTCTTGTATGAGATGCT 814
 Qy 915 GTATGGCCTGCGCCCTTTTATAGCCGAAACACAGCTGAAATGTAGACAACTTCTGAA 974
 Db 815 GTATGGCCTGCGCCCTTTTATAGCCGAAACACAGCTGAAATGTAGACAACTTCTGAA 874
 Qy 975 CAAAGCCTCTCCAGCTGAAACCAATATTACAAATTCGCAAGACACCTCTCTGAGGCGCT 1034
 Db 875 CAAAGCCTCTCCAGCTGAAACCAATATTACAAATTCGCAAGACACCTCTCTGAGGCGCT 934
 Qy 1035 CCTGCAGAGGACAGACAAAGCGCTCGGGGCCAAGGATGACTTTCATGAGATTAAAG 1094
 Db 935 CCTGCAGAGGACAGACAAAGCGCTCGGGGCCAAGGATGACTTTCATGAGATTAAAG 994
 Qy 1095 TCATGTCTTCTCTCTTAACTGGAATGATCTCATTATTAAGAGATTACTCCCC 1154
 Db 995 TCATGTCTTCTCTCTTAACTGGAATGATCTCATTATTAAGAGATTACTCCCC 1054
 Qy 1155 TTTTAAACCAAAATGTGAGTGGGCCCAACGACCTTACCGGCTTTGACCCGAGTTTACCGA 1214
 Db 1055 TTTTAAACCAAAATGTGAGTGGGCCCAACGACCTTACCGGCTTTGACCCGAGTTTACCGA 1114
 Qy 1215 AGAGCCTGTCCCCAACTCCATTGGCAAGTCCCCGTGACAGCTCTCTGTCACAGCCAGCGT 1274

Db 1115 AGAGCCTGTCCTCCCACTCCATTGGCAGTCCCTGACAGGCTCTCTGTCACAGCCAGCGT 1174
 Qy 1275 CAAGGAAGTCGCGAGGCTTTCTTAGGCTTTTCTATGCGCTTCCACAGGACTCTTTCTT 1334
 Db 1175 CAAGGAAGTCGCGAGGCTTTCTTAGGCTTTTCTATGCGCTTCCACAGGACTCTTTCTT 1234
 Qy 1335 CTGA 1338
 Db 1235 CTGA 1238

RESULT 9

AAA46592
 ID AAA46592 standard; DNA; 2365 BP.

XX
 AC AAA46592;

XX 25-SEP-2000 (first entry)

XX DNA encoding a rat serum and glucocorticoid induced protein kinase.

XX Protein kinase; Pkh1; Pkh2; Ypk1; Yrk2; protein kinase B-alpha;
 KW serum and glucocorticoid induced protein kinase; SGK; PKBalpha;
 KW 3-phosphoinositide-dependent protein kinase-1; PDK1; fungal infection;
 KW thrush; cancer; diabetes; obesity; antifungal; Candida infection; ss.

XX Rattus sp.

XX Key Location/Qualifiers

FF 1..1288

FT /*tag= a

FT /product= "serum and glucocorticoid induced protein

FT kinase (SGK)"

FT /transl_except= (pos: 1, aa: Thr)

FT /note= "the codon encoding Met at position 1 and

FT Pro at position 318 are not given"

XX WO200036135-A2.

XX 22-JUN-2000.

XX 14-DEC-1999; 99WO-GB04228.

XX 14-DEC-1998; 98US-0112114.

XX (MEDI-) MEDICAL RES COUNCIL.

PA (REGC) UNIV CALIFORNIA.

XX Thorne JW, Alessi DR, Torrance PD, Casamayor A;

XX WPI; 2000-442391/38.

XX P-PSDB; AAY93530.

XX Screening method identifying compounds which modulate protein kinase

XX activity for use in treating fungal infections and cancer -

XX Disclosure; Fig 12; 155pp; English.

XX The present sequence encodes a rat serum and glucocorticoid induced
 CC protein kinase (SGK). The specification describes a screening method
 CC to identify a compound which modulates the activity of protein kinases
 CC from different sources, using host yeast cells. The method is used to
 CC identify a compound which modulates (inhibits) the activity of a
 CC protein kinase. Pkh1 or Pkh2 phosphorylate and activate Ypk1, Yrk2,
 CC SGK or protein kinase B-alpha (PKBalpha). 3-phosphoinositide-dependent
 CC protein kinase-1 (PDK1) is used to phosphorylate and activate Ypk1 and
 CC Yrk2 or SGK but not PKBalpha or p70S6 kinase. Compounds identified by
 CC the methods are used to treat fungal infections e.g. thrush, and to
 CC treat cancer. To treat cancer, the compounds inhibit PKB, PDK1 or the
 CC activation of PKB by PDK1. Compounds which activate PKB or PDK1 can be
 CC used in the treatment of diabetes or obesity, and compounds which
 CC inhibit a fungal functional homologue of PDK1 (Pkh1 or Pkh2) or SGK

CC (Ypk1 or Yrk2) can be used as an antifungal agent to treat Candida
 CC infections, e.g. thrush.
 XX Sequence 2365 BP; 591 A; 580 C; 518 G; 676 T; 0 other;
 SQ Query Match 73.5%; Score 983; DB 21; Length 2365;
 Best Local Similarity 88.3%; Pred. No. 7.3e-280;
 Matches 1080; Conservative 0; Mismatches 140; Indels 3; Gaps 1;
 Qy 116 TGGCTTTTCATGAAGCAGAGGAGGATGGGTCTGAACGACTTTTATTCAGAGATTCGCAATA 175
 Db 69 TCGCTTTTCATGAAGCAGAGAGGATGGGCTGAACGATTTTATTCAGAGATTCGCAACA 128
 Qy 176 ACTCCTATGATGCAACACCCCTGAAAGTTTCAGTCCATCTTGAAGATCTCCCAACCTCAGG 235
 Db 129 ACTCCTATGATGCAACACCCCTGAAAGTTTCATCTTATTTGAAATCTCCCAACCTCAGG 188
 Qy 236 AGCCTGAGCTTATGAATGCCAACCCCTTCTCTCCACCAAGTCTTCTCAGCAAAATCAACC 295
 Db 189 AGCCCGAAGTTTATGAACGCCAACCCCTCACCTCTCCAAGTCCCTCTCAACAAATCAACC 248
 Qy 296 TTGGCCCGTCCATCTCTGATGCTAAACCATCTGACTTTTCACTTTTGAAGTATCG 355
 Db 249 TGGGTCCATCTCTCAATCCCAACCCCTCTGACTTCCACTTCTTTGAAAGTATCG 308
 Qy 356 GAAAGGCGAGTTTGGAAAGGTTTCTTAGCAAGCACAAAGGCGAGAGAGTCTTCTATG 415
 Db 309 GAAAGGCGAGTTTGGAAAGGTTTCTTAGCAAGGCGAAGGCGAGAGAGTCTTCTATG 368
 Qy 416 CAGTCAAAAGTTTTACAGAAAGCAATCTGAAAGAAAGAGAGAGAGATTTATATGT 475
 Db 369 CCGTCAAAAGTTTTGCAAGAAAGCCATCTTGAAGAAAGAGAGAGAGATTTATATGT 428
 Qy 476 CGGAGCGGAATGTTCTGTTGAAGATGTGAAGCACCCTTTCTGTTGGGCTTCACTTCT 535
 Db 429 CAGAGCGCAATGTTCTGTTGAAGATGTGAAGCACCCTTTCTGTTGGGCTTCACTTCT 488
 Qy 536 CTTTCCAGACTGCTGACAAATTTGTTCTTAGACTACATTAATGTTGGAGAGTGT 595
 Db 489 CTTTCCAGACTGCTGACAAATCTTCTTCTTAGACTACATTAATGTTGGAGAGTGT 548
 Qy 596 TCTACCATCTCCAGAGGGAAACGCTGCTTCTGGAAACCCGCGCTCTTCTATGCTGCTG 655
 Db 549 TCTACCATCTCCAGAGGGAGCGCTGCTTCTGGAAACCCGCTGCTCTTCTACGACGCTG 608
 Qy 656 AAATAGCCAGTGGCTTGGGCTACCTGCAATCTGAAATCTTATAGAGACTTAAAC 715
 Db 609 AAATAGCCAGTGGCTTGGGCTTATCTGCACTCCCTAAACATCGTTTATCGAGACTTAAAC 668
 Qy 716 CAGAGAAATTTTGTAGATTTCAGGGACACATTTGCTTCTTACTGACTTCGGACTCTGCA 775
 Db 669 CAGAGAAATTTTCTCTAGACTCAGGGGACACATCTCTCTACTGACTTTGGGCTCTGCA 728
 Qy 776 AGGAGAAATTTGAACACAAACAGCAACATCCACCTTCTGTGGCAGCGCGAGTATCTCG 835
 Db 729 AGGAGAAATCTGAGCAACATGGGACAACTCCACCTTCTGTGGCAGCGCTGAGTATCTCG 788
 Qy 836 CACCTGAGTGTCTTATAGCAGCCTTATGACAGGACTGTGGACTGGTGGTGGCTGGGAG 895
 Db 789 CTCCTGAGTGTCTTATAGCAGCCTTATGAGGCTGGGCTGGTGGTGGCTGGGAG 848
 Qy 896 CTGCTTGTATGAGTGTCTTATGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGAG 955
 Db 849 CTGCTTGTATGAGTGTCTTATGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGAG 908
 Qy 956 TGTACGACAACTTCTGAACAAAGCTCTCTCAGCTGAAACCAATATATACAAATTCGCGAA 1015
 Db 909 TGTATGACAAATTTCTGAACAAAGCTCTCTCAGCTGAAACCAATATATACAACTCAGCAA 965
 Qy 1016 GACACCTCTGGGAGGCTCTTCTGCAAGGAGGAGGAGGAGGCTCGGGGCGCAAGATG 1075
 Db 966 GGCACCTGTGGAGGCTCTTCTGCAAGGAGGAGGAGGAGGCTCGGGGCGCAAGATG 1025

Qy	1076	ACTTCATGGAGATTAAAGAGTCATGCTCTTCTCTCTTAATAACTGGATGATCTCAATTA	11335
Db	1026	ACTTTATGGAGATTAAAGAGTCATATTTCTCTCTTTGATTAACTGGATGATCTCAATTA	1085
Qy	1136	ATAAGAAGATTACTCCCCCTTTTAAACCAATGTGAGTGGGCCCAACGACTACGGCACT	1195
Db	1086	ATAAGAAGATCACGCCGCCCATTTAAACCAATGTGAGGGGCCCACTGACCTTCGGCACT	1145
Qy	1196	TTGACCCCGAGTTTACCGAAGAGCCTGTCCCAAATCTCAATGGCAAGTCCCTTGACAGCG	1255
Db	1146	TTGATCCCGAGTTTACTGAGAGCGCGTCCCACTCATCGGCGCATCCCTTGACAGCA	1205
Qy	1256	TCCTCGTACAGCCAGCGTCAAGAAGCTGCCGAGGCTTTCTTATAGGCTTTTCTTATGCGC	1315
Db	1206	TCCCTTGTCACAGCCAGTGTGAAGAGCGCGGGAAGCTTCTCTTGGCTTCTCTATGCC	1265
Qy	1316	CTCCCACGGACTCTTTCTCTGA	1338
Db	1266	CTCCTATGGACTCTTCTCTGA	1288

RESULT 10

RESOLVED TO
AA444640

ID AAF44640 standard: cDNA: 2432 BP.

AC AAF44640:

27-MAR-2001 (first entry)

DE Novel protein kinase cDNA, SEQ ID NO: 19.

Human, mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
immunosuppressive; cardiac; renal; antiinflammatory; antilasthmatic;
dermatological; antidiabetic; infertility; gene therapy; vaccine;
immune disorder; cardiovascular disease; neurodegenerative disease;
cancer; autoimmune disorder; stroke; inflammatory bowel disease;
inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.

OS Mus musculus.

PN WO200073469-A2.

PD 07-DEC-2000.

26-MAY-2000: 2000WO-US14842.

PR 28-MAY-1999: . 99US-0136503.

PA (SUGE-) SUGEN INC.

PI Plowman GD, Martinez R, Whyte D, Sudersanam S;

DR WPI: 2001-032161/04.

DR P-PSDB; AAB65614.

PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT treating immune-related diseases and disorders, cardiovascular disease,
PT neurodegenerative diseases and/or cancers -

PS Disclosure: Fig 2: 310pp: English.

The present sequence encodes a novel protein kinase. The nucleic acids and the protein kinases they encode may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase antagonists may also be used to down regulate kinase expression and activity. Diseases related to kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, complications of organ transplantation, myocardial infarction.

Db 1045 GGCACCTCTGGAGGCTCTCTGAGAGGACCGGACCAAGAGGCTGGTGCCAAAGGATG 1104
 Qy 1076 ACTTCAGGAGATTAAAGATCATGCTTCTTCTCTTAATTAAGTGGATGATCTCATTA 1135
 Db 1105 ACTTTATGGAGATTAAAGATCATATTTTCTTCTTTAAATTAAGTGGATGATCTCATCA 1164
 Qy 1136 ATAAGAAGATTACTCCCTCTTTAAACCAATGAGTGAGTGAGGCGCAACGACCTAGGCAC 1195
 Db 1165 ATAAGAAGATTACACCCCATTTAAACCAATGAGTGAGTGAGGCGCAACGACCTAGGCAC 1224
 Qy 1196 TTGACCCGAGTTTACCAAGAGGCTGTCCCAACTCCATTTGGCAAGTCCCTCGACAGCG 1255
 Db 1225 TCGATCCGAGTTTACCGAGGCGGTCCCGAGCTCCATCGGAGTCCCTCGACAGCA 1284
 Qy 1256 TCCTCGTCAGCCAGCGTGAAGAGCTGCGGAGGCTTCTTAGGCTTTCTTCTATGCGC 1315
 Db 1285 TCCTTGTACGGCCAGTGTGAAGAGCAGCAGAGAGCTTCTCTGGCTTCTCTATGCGC 1344
 Qy 1316 CTCACCGGACTCTTCTCTCTGA 1338
 Db 1345 CTCTGTGGATTCTTCTCTCTGA 1367

RESULT 11

AAS44987
 ID AAS44987 standard; cDNA; 1366 BP.

XX AAS44987;

AC AAS44987;

DT 18-DEC-2001 (first entry)

XX cDNA encoding novel human secretory protein, Seq ID No 68.

XX Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KW myotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
 KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;
 KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KW fertility; analgesic; pain; antigen; ss.

XX Homo sapiens.

XX W0200166689-A2.

XX 13-SEP-2001.

XX 05-MAR-2001; 2001WO-US04942.

XX 07-MAR-2000; 2000US-0519705.

PR 19-MAY-2000; 2000US-0574454.

PR 17-JUN-2000; 2000US-0596193.

PR 14-JUL-2000; 2000US-0616847.

PR 19-SEP-2000; 2000US-0665363.

PR 20-OCT-2000; 2000US-0693267.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;

PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;

XX WPI; 2001-589934/66.

XX P-PSDB; AAU28087.

XX Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders -
 XX Claim 1; SEQ ID No 68; 107pp; English.

CC The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I), (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions,
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biorhythms or circadian cycles of rhythms, CC
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC analgesic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAS44920-AAS45295 represent novel human secreted protein
 CC coding sequences of the invention.
 XX

XX SQ Sequence 1366 BP; 331 A; 374 C; 377 G; 284 T; 0 other;

Query Match 39.4%; Score 527.2; DB 22; Length 1366;
 Best Local Similarity 69.5%; Pred. No. 3.5e-145;
 Matches 734; Conservative 0; Mismatches 313; Indels 9; Gaps 1;
 Qy 261 TTCTCTCCACCAAGTCTTCTCAGCAATCAACCTTGGCCGCTCTCAATCCTCATGC 320
 Db 213 TCCACAGCCCTCCAGGGCCAAATGGGAACATCAACCTGGGGCTTCCAGCAACCAATGC 272
 Qy 321 TAAACCATCTGACTTTTCACTTCTTGAAGTGATCGGAAGGGCAGTTTGGAAAGCTTCT 380
 Db 273 CCAGCCCGGACTTTCGACTTCTCAAAGTCAATCGGCAAGGGAAGTACGGGAAGTCTCT 332
 Qy 381 TCTAGCAAGACACAAGGCAGAGAAGTGTCTATGCAGTCAAAAGTCTTACAGAGAAGAAC 440
 Db 333 ACTGGCCCAAGCGCAAGTCTGATGGGCGTCTTATGCAGTGAAGTACTACAGAAAAGTC 392
 Qy 441 AATCTGAAAAGAAAGAGAGAGAGCATATTATGTCGGAGCGGAATGTTCTGTGTAAGAA 500
 Db 393 CATCTTAAAGAAAG 452
 Qy 501 TGTGAAGCAGCCCTTCTCTGGTGGGCTTCACTTCTTCTTCCAGACTGCTGACAAATGTA 560
 Db 453 CGTGGCGCACCCCTTCTCTGGGCTTCCGCTACTCTTCCAGACACCTTGAAGAGTCTTA 512
 Qy 561 CTTTGTCTTAGACTACATTAATGTTGGAGAGTGTGTTCTACCATCTCCAGAGGGAAGCTG 620
 Db 513 CTTCGTGCTCGACTATGTCAACGGGGAGAGAGTCTTCTTCCACCTCGAGGGAGCGCG 572
 Qy 621 CTTCCTGGAAACCAAGGCTCGTTTCTATGCTGCTGAAATAGCCAGTGCCTTGGGCTACCT 680
 Db 573 GTTCTCTGGAGCCCGGGCCAGGTTCTACGCTGTGAGGTGGCCAGGCCATTGGCTACCT 632
 Qy 681 GCATTCACCTGACATCGTTTATAGAGACTTAAACCCAGAGAGATATTTTCTAGATTACA 740
 Db 633 GCACCTCCCTCAACATCATTTACAGGGATCTGAAACCCAGAGAGAACTTCTCTTGGCTGCCA 692
 Qy 741 GGGACACATTGTCTTACTGACTTTCGAGTCTCGAAGGAGAACATTTGAACACACAGCAC 800

Db 693 GGGACAGTGGTGTGAGGATTTGGCCCTTCGACGGAAGGTGTAGAGCCTGAAGACAC 752
 Qy 801 AACATCCACCTTCTGTGGCAGCGCGAGTATCTGACACCTGAGGTGCTTCATAGCAGCC 860
 Db 753 CACATCCACATCTGTGTACCCCTGAGTACTTGGCACCTGAGTCTTCGGAAGAGCC 812
 Qy 861 TTATGACAGACTGTGAGTGGTGGTGGTGGAGCTGTCTTGTATGAGATGCTGTATGG 920
 Db 813 TTATGATCGAGCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 872
 Qy 921 CCTGCCCTTTTATAGCCGAAACACAGCTGGAATGTAGCAGACACATCTGTAACAGCC 980
 Db 873 CCTGCCCTTTTACAGCCAAAGATGTATCCAGATGTATGAGAACATCTTGACACAGCC 932
 Qy 981 TCTCCAGCTGAAACCAATATTACAAATTCGCAAGACACCTCTGAGGCGCTCTCTGCA 1040
 Db 933 GCTACAGATCCCGAGCGCGACAGTGGCGCTGTGACCTCTGCAAGCTTCTCCA 992
 Qy 1041 GAAGGACAGACAAAGCGGTGGGGCAAGGATGACTTCAATGAGAGATTAGAGTCAATG 1100
 Db 993 CAAGGACAGAGCGAGCGGTGGGCTCCAAAGCAGACTTTCTTGAGATTAAAGAACCATGT 1052
 Qy 1101 CTTCCTCTCTTAATTAAGTGGGATGATCTCATTAATAAGAGATTACTCCCTTTTAA 1160
 Db 1053 ATTCTTCAGCCCCATAAAGTGGGATGACCTGTATCCAAAGAGGTAACTCCACCTTCAA 1112
 Qy 1161 CCCAAATGTAGTGGGCGCAAGCAGCTACGCGACTTTGACCCCGAGTTTACCGAAGAGCC 1220
 Db 1113 CCCAAATGTAGCAGGACTGCTGACTTGAAGCATTTTGACCCAGAGTTACCCAGGAGC 1172
 Qy 1221 TGTCCCAACTCCATTTGGCAAGTCCCTGACAGCGTCTCTGTCACAGCCAGCGTCAAGGA 1280
 Db 1173 TGTGTCAAGTCCATTTGGTGTACCCCTGACACTGT-----GGCCAGCAGCTCTGG 1223
 Qy 1281 AGTGGCGAGGCTTCTTAGGCTTTCTTATGGCC 1316
 Db 1224 GGCCTCAAGTGCATTCCTGGGATTTCTTATGGCC 1259

RESULT 12
 AAF44737
 ID AAF44737 standard; cDNA; 1812 BP.
 AC AAF44737;
 DT 27-MAR-2001 (first entry)
 DE Novel protein kinase cDNA, SEQ ID NO: 118.

Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
 immunosuppressive; cardiac; renal; antiinflammatory; antiaesthetic;
 dermatological; antidiabetic; antifertility; gene therapy; vaccine;
 immune disorder; cardiovascular disease; neurodegenerative disease;
 cancer; autoimmune disorder; stroke; inflammatory bowel disease;
 inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.
 Homo sapiens.
 OS
 XN WO200073469-A2.
 XX
 XX 07-DEC-2000.
 XX
 XX 26-MAY-2000; 2000WO-US14842.
 XX
 XX 28-MAY-1999; 99US-0136503.
 XX
 XX (SUGEN-) SUGEN INC.
 XX
 XX Plowman GD, Martinez R, Whyte D, Sudrean S;
 XX
 XX WPI; 2001-032161/04.
 DR P-PSDB; AAB65708.

XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
 PT treating immune-related diseases and disorders, cardiovascular disease,
 PT neurodegenerative diseases and/or cancers -
 XX Disclosure; Fig 2; 310pp; English.
 XX
 XX The present sequence encodes a novel protein kinase. The nucleic acids
 CC and the protein kinases they encode may be used in the treatment and
 CC diagnosis of diseases associated with inappropriate kinase expression
 CC such as immune-related diseases and disorders, cardiovascular disease,
 CC neurodegenerative diseases and/or cancers. The nucleic acids and
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays. The kinase polypeptides may be used as antigens in the production
 CC of antibodies of kinase expression and activity. Anti-kinase antibodies
 CC and kinase antagonists may also be used to down regulate kinase
 CC expression and activity. Diseases related to kinase expression and
 CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
 CC disorders, complications of organ transplantation, myocardial infarction,
 CC immune disorders, cardiomyopathies, strokes, renal failure,
 CC oxidative-stress related disorders, chronic inflammatory bowel disease,
 CC chronic inflammatory pelvic disease, multiple sclerosis, asthma,
 CC osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and
 CC reproductive disorders.
 XX
 SQ Sequence 1812 BP; 461 A; 470 C; 470 G; 411 T; 0 other;
 Query Match 39.4%; Score 527.2; DB 22; Length 1812;
 Best Local Similarity 69.5%; Pred. No. 4.1e-145;
 Matches 734; Conservative 0; Mismatches 313; Indels 9; Gaps 1;
 Qy 261 TTCTCTCCACCAAGTCTTCTCAGCAATCAACCTTGGCCCTGCTCCATCTCATGC 320
 Db 117 TCCACAGCCCTCCAGGCCAATGGGAACATCAACCTGGGCGCTTCAGCCAACTATGC 176
 Qy 321 TAAACCATCTGACTTTTCACTTCTTGAAGTATCGGAAGGCGAGTTTGGAAAGTTCT 380
 Db 177 CCAGCCCGAGGACTTCGACTTCTCAAAGTCACTCGGCAAGGGAAGTACCGGAGGTCT 236
 Qy 381 TCTAGCAAGACACAAAGGAGAAAGTGTCTATGAGTCAAAAGTTTACAGAAAGAAAGC 440
 Db 237 ACTGGCCAGCGAAGTCTGTATGGGCGTCTATGAGTCAAGGTACTACAGAAAGATC 296
 Qy 441 AATCTCTGAAAGAAAGAGAGAGCATATATGTCCGAGCGGAATGTCTGTGTGAAGAA 500
 Db 297 CATCTTAAAGAAAG 356
 Qy 501 TGTGAAGACCCCTTCTGTGTGGGCTTCACTTCTCTTCCAGACTGCTGACAAATGTGA 560
 Db 357 CGTGGCGACCCCTTCTGTGGGCGTCTGCTTCCAGACTGCTGCTTCCAGAGCTCTA 416
 Qy 561 CTTTGTCTAGACTACATTAATGCTGAGAGTGTCTTCTACCATCTCCAGAGGAAAGCTG 620
 Db 417 CTTCTGTCTGACTATGTCAACGGGGAGAGTCTTCTTCCAGCTGAGGAGAGAGAG 476
 Qy 621 CTTCTGTGAAACAGCGGCTCGTTTCTATGCTGTGAAATAGCCAGTGGCTTGGCTACCT 680
 Db 477 GTTCTGGAGCCCGGCGGAGGTTTCTACGCTGTGAGTGGCCAGCGCAATTGCTACCT 536
 Qy 681 GCATTCAGTGAACATCGTTTATAGAGACTTAAACACAGAGAAATATTTGCTAGATTACA 740
 Db 537 GCATCTCCCTCAACATCATTTACAGGGATCTGAAACACAGAGAAATCTCTTGGAGCTCCA 596
 Qy 741 GGGACACATGTCTTACTGACTTCGAGCTCTCAAGGAGAAACATTGAACACACACACAC 800
 Db 597 GGGACACGTTGCTGTGACGGATTTTGGCTCTTCAAGGAAAGGTGTAGAGCTTGAAGAC 656
 Qy 801 AACATCCACCTTCTGTGGCAGCGCGAGTATCTCGACCTCGAGTGTCTTCAATAGCAGCC 860
 Db 657 CACATCCACATCTGTGGTACCCCTGAGTACTTGGCAGCTGAGTGTCTCGGAAGAGCC 716
 Qy 861 TTATGACAGACTGTGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 920

Db 717 TTATGATGAGCAGTGACTGGTGGTCTTTGGGGCAGTCTCTCTACAGAGATGCTCCATGG 776
 Qy 921 CCTGCCGCTTTTATAGCCGAACACAGCTGAAATGTACGACAACTTCTGAACAAGCC 980
 Db 777 CCTGCCGCTTTTATAGCCGAACAGATGTATCCAGATGTATGAGAACATCTGCACAGCC 836
 Qy 981 TCTCCAGCTGAACCAATATTACAAATTCGCAAGACACCTCTCTGGAGGGCTCTCTGCA 1040
 Db 837 GCTACAGATCCCGAGCGCCGACAGTGGCGCTGTGACCTCTCTGCAAGCTTCTCCA 896
 Qy 1041 GAAGGACAGACAAAGCGCTCGGGCCAAAGGATGACTTCTATGAGATTAAGAGTATGT 1100
 Db 897 CAAGGACAGAGCGAGCGCTGGCTCTCAAGCAGAGCTTTCTTGAGATTAAGAACATGT 956
 Qy 1101 CTCTCTCTCTTAATTAACCTGGGATGATCTCAATTAAGAGATTAACCTCTCTTTAA 1160
 Db 957 ATTCTTCAGCCCACTAACTGGGATGACCTGTACCAAGAGGCTAACTCCACCTTCAA 1016
 Qy 1161 CCCAAATGTGAGTGGGCGCCCAACGACCTACGCGACTTTGACCCGAGTTTACCGAAGAGCC 1220
 Db 1017 CCCAAATGTGACAGGACCTGCTGACTTGAAGCATTTTGACCCAGAGTTACCCAGGAAGC 1076
 Qy 1221 TGTCCCACTCAATGGGAGTCCCTTGACAGGCTCTCTGTCACAGCCAGCGTCAAGGA 1280
 Db 1077 TGTGTCCCAAGTCCATTTGGCTGTACCCCTGACACTGT-----GGCCAGCAGCTCTGG 1127
 Qy 1281 AGTGGCCGAGGCTTTCTCTAGGCTTTTCTCTATGGCC 1316
 Db 1128 GGCCTCAAGTGCATTTCTCTGGGATTTCTTATGGCC 1163

RESULT 13

AAD36141

ID AAD36141 standard; DNA; 1812 BP.

AC AAD36141;

XX 09-AUG-2002 (first entry)

XX Human serum and glucocorticoid-induced protein kinase, SGK2-alpha gene.

XX Human; cytostatic; antisense gene therapy; screening; protein kinase;
 KW cancer; liver; colon; tumour; inflammation; arthritic synovium; gene;
 KW serum and glucocorticoid-induced protein kinase; SGK2-alpha; enzyme; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FH 88..1191

FT /*tag= a

FT /product= "Human SGK2-alpha protein"

XX W0200224947-A2.

PN 28-MAR-2002.

PD 20-SEP-2001; 2001WO-IB02237.

PF 20-SEP-2000; 2000US-233999P.

XX 02-OCT-2000; 2000US-237419P.

PR 02-OCT-2000; 2000US-237423P.

PR 04-OCT-2000; 2000US-238558P.

PR 10-MAY-2001; 2001US-290555P.

XX (KINE-) KINETEK PHARM INC.

PA (UYBR-) UNIV BRITISH COLUMBIA.

XX Yoganathan T, Delaney AD;

XX WPI; 2002-394145/42.

XX P-PSDB; AAE22765.

XX Diagnosing cancer, comprises determining the upregulation of expression

PT of a nucleic acid sequence encoding a protein kinase or upregulation of
 expression of the protein kinase, in the cancer
 XX Claim 16; Page 65-66; 87pp; English.

CC The invention relates to a method for screening biologically active agent
 CC that modulates cancer associated protein kinase function. The invention
 CC also relates to a method for diagnosing cancer comprising determining the
 CC upregulation of expression of a nucleic acid sequence encoding a protein
 CC kinase. The method is useful for diagnosing cancer. A protein kinase is
 CC useful for screening biological agents that modulate cancer associated
 CC protein kinase function. Downregulating the activity of protein kinase is
 CC useful for inhibiting the growth of a cancer cell, e.g. liver or colon
 CC cancer. A nucleic acid encoding protein kinase is useful to screen biopsy
 CC derived tumours and inflammatory samples such as arthritic synovium, for
 CC amplified DNA in the cell or increased expression of corresponding mRNA
 CC or protein and is also useful to detect differences in expression levels
 CC such as molecular weight, amino acid and nucleotide sequences between the
 CC two cells. The present sequence is human serum and glucocorticoid-induced
 CC protein kinase, SGK2-alpha gene.

XX Sequence 1812 BP; 461 A; 470 C; 470 G; 411 T; 0 other;

Query Match 39.4%; Score 527.2; DB 24; Length 1812;
 Best Local Similarity 69.5%; Pred. No. 4.1e-145;
 Matches 734; Conservative 0; Mismatches 313; Indels 9; Gaps 1;

Qy 261 TTCTCTCTCCACCAAGTCTTCTTCAGCAATCACTTGGCCCTGCTCCCAATCCTCATGC 320
 Db 117 TCACAGCCCTCCAGGGCAATGGGAACATCACTTGGGGCTTCAGCCCAACCAATGC 176
 Qy 321 TAAACCATCTGACTTTTCACTTTTGAAGTGTATCGGAAGGGCAGTTTGGAAAGTTCT 380
 Db 177 CCAGCCCAAGGACTTCGACTTCTCAAGTATCGCAAGGGAAGTACGGGAAGTCTCT 236
 Qy 381 TCTAGCAAGACACAAGGCAGAGAAGTGTCTATGAGTCAAAAGTCTTTCAGAAAGAAC 440
 Db 237 ACTGGCCAAAGCGCAAGTCTGTGGGCGTTCTATGCAAGTGAAGTACTACAGAAAAATC 296
 Qy 441 AATCCTGAAAGAAAGAGAGAGAGATATATATGCGAGCGGAATTTCTGTGTAGAA 500
 Db 297 CATCTTTAAAGAAAG 356
 Qy 501 TGTGAAGACCCCTTCTCTGGTGGCTTCACTTCTCTTCCAGACTGTGTACAAATTTGA 560
 Db 357 CGTGGCGACCCCTTCTCTGGTGGCTTCTCTTCCAGACCTGAGAGGCTCTA 416
 Qy 561 CTTTGTCTTAGACTACATTAATGGTGGAGAGTTGTTTCTACCATCTCCAGAGGAAGCTG 620
 Db 417 CTTCTGTCTGACTATGTCAACGGGGAGAGAGTCTTCTTCCACTGCGAGGGAGCGCG 476
 Qy 621 CTTCTGTGAACACAGGGCTCGTTTCTATGCTGTGAATAGCCAGTCCCTTGGGCTACCT 680
 Db 477 GTTCTGTGAGAGCCCGGGCCAGGTTCTACGCTGTGAGTGGCCAGCCATTGGCTACCT 536
 Qy 681 GCATTCACTGAACATCGTTTATAGAGACTTAAACACAGAGAAATTTTGTAGATTACCA 740
 Db 537 GCACTCCCTCAACATCATTTACAGGATCTGAAGCCAGAGAACATTTCTTTGACTGCCA 596
 Qy 741 GGGACACATTTGCTTACTGACTTCGAGCTCTGCAAGAGAGAACATTTGAACACACAGCAC 800
 Db 597 GGGACACAGTGTGCTGACGATTTTGGCTCTCTCAAGGAAGGTGTAGAGCTTGAAGACAC 656
 Qy 801 AACATCCACTTCTGTGGACCGCCGAGTATCTCGCACCTGAGTGTCTTATAGAGAGCC 860
 Db 657 CACATCCACATTTCTGTGTGTAACCCCTGAGTACTTGGCACCTGAAAGTCTTCGGAAGAGCC 716
 Qy 861 TTATGACAGAGCTGTGGACTGTGGTGGCTCTGGAGAGTGTCTTGTATGAGATGCTGTATGG 920
 Db 717 TTATGATCGAGCAGTGGAGTGTGGTGGTGTCTTGGGGCAGTCTCTACGAGATGCTCCATGG 776
 Qy 921 CTTGCCGCTTTTATAGCCGAAACAGCTGAAATGTATAGCAACATTTCTGAACAGGCC 980

Db 777 CTGCGCCGCTTCTACAGCCAGAGTGTATCCAGATGTATGAGAAATTTCTGCACAGCC 836
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 Qy 1041 GAAGCAGGACAAAGCGGCTCGGGGCAAGGATGACTTCTATGGAGATTAGAGTCTATGT 1100
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RESULT 14

AAA27856
 ID AAA27856 standard; cDNA; 1834 BP.

XX AAA27856;

XX 12-SEP-2000 (first entry)

XX Human serum and glucocorticoid-induced protein kinase 2-alpha cDNA.

XX Serum and glucocorticoid-induced protein kinase 2; SGK2-alpha;
 KW human; phosphorylation; cancer; diabetes; ischaemia; therapy; ss.
 OS Homo sapiens.

XX Key Location/Qualifiers
 FT CDS 88..1191
 FT /*tag= a

XX W0200035946-A1.

XX 22-JUN-2000.

XX 14-DEC-1999; 99WO-GB04232.

XX 14-DEC-1998; 98US-0112217.

XX 19-AUG-1999; 99GB-0019676.

XX (UYDU-) UNIV DUNDEE.

XX Cohen P, Kobayashi T, Deak M;

XX WPI; 2000-442364/38.

XX P-PSDB; AAY95275.

XX Modulation of serum and glucocorticoid-induced protein kinase (SGK) by
 PT phosphorylation with 3-phosphoinositide-dependent protein kinase-1
 PT (PK1) or dephosphorylation, useful for treatment of cancer, diabetes
 PT and ischemic diseases -

XX Disclosure; Page 26-27; 127pp; English.

XX The present sequence is that of cDNA coding for human serum and
 CC glucocorticoid-induced protein kinase (SGK) isoform 2-alpha (see
 CC AAY95275). SGK (see AAY95279) was initially identified as a
 CC glucocorticoid and osmotic stress-responsive gene. Novel isoforms,

CC SGK2 and SGK3, were isolated from EST database searches, and 2
 CC splice variants of SGK2, i.e. SGK2-alpha and -beta (see AAY95276),
 CC which contains an extra 60 N-terminal residues, were identified.
 CC SGK2-alpha is expressed in liver, kidney, pancreas and brain. It
 CC is activated by phosphorylation in a similar manner to SGK. The
 CC invention provides methods of activating SGK activity by
 CC phosphorylation using 3-phosphoinositide-dependent protein kinase-1
 CC (PK1), and of reducing the activity of SGK by dephosphorylation.
 CC The invention also provides a method of identifying a compound that
 CC modulates the activity of SGK. Such compounds are useful for
 CC treating patients requiring modulation of SGK, such as patients
 CC with cancer, diabetes or ischaemic disease.

XX SQ Sequence 1834 BP; 483 A; 470 C; 470 G; 411 T; 0 other;

Query Match 39.4%; Score 527.2; DB 21; Length 1834;
 Best Local Similarity 69.5%; Pred. No. 4.1e-145;
 Matches 734; Conservative 0; Mismatches 313; Indels 9; Gaps 1;

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 Db 297 CATCTTAAAG 356
 Qy 501 TGTGAAGACACCTTCTCTGTTGGGCTTCACTTCTTCTTCCAGACTGTGACAAATGTA 560
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 Db 477 GTTCTGGAGCCCGCGGCGAGGTTCTACGCTGCTGAGTGGCCAGCGCATTTGGCTACCT 536
 Qy 681 GCAATCACTGAACATCGTTTATAGAGACTTAAACCCAGAGAAATATTTTGTAGATTACA 740
 Db 537 GCACCTCCCTCAACATCATTTACAGGAGTCTGAAACCAGAGAGAGAGAGAGAGAGAG 596
 Qy 741 GGGACACATTTCTTACTGACTTCGAGCTCTGCAAGGAGAGAGAGAGAGAGAGAGAGAG 800
 Db 597 GGGACACGTTGCTGACCGGATTTTGGCCCTCTGCAAGGAGAGAGAGAGAGAGAGAGAG 656
 Qy 801 AACATCCACTCTGTGGCAGCGCGAGTATCTCGCACCTCGAGGTGCTTCTATAGAGAGCC 860
 Db 657 CACATCCACATTTCTGTGTACCCCTGAGTACTTGGCACCTGAGTCTTCTGGAAGAGCC 716
 Qy 861 TTATGACAGGACTGTGGACTGTGTGCTGCTGGAGCTGTCTTGTATGAGATGCTGTATGG 920
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 Qy 981 TCTCAGAGTGAACCAAAATATTACAAATTCGCAAGACACCTCTCGAGGGCTCTCTGCA 1040
 Db 837 GCTACAGATCCCGGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 896
 Qy 1041 GAAGGACAGGACAAAGCGCTCGGGCCCAAGGATGACTTTCATGGAGATTAAAGAGTCTGT 1100

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Db	1389	TGTTCCAAAGTCCATTGGCTGTACCCCTGACACTGT-----GGCCACGACGCTCTGG	1439
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Job time : 247 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 06:39:20 ; Search time 2375 Seconds
(without alignments)
16395.602 Million cell updates/sec

Title: US-10-067-977-1

Perfect score: 1338
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

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4: gb.om.*
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6: gb.pat.*
7: gb.ph.*
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10: gb.ro.*
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17: em.hum.*
18: em.in.*
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41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1221.4	91.3	2364	9	AK098509 Homo sapi
2	1221.4	91.3	2382	9	AF153609 Homo sapi
3	1221.4	91.3	2382	9	BC001263 Homo sapi
4	1219.8	91.2	2311	6	AR151390 Sequence
5	1219.4	91.1	3196	9	AK055077 Homo sapi
6	1218.2	91.0	1296	6	AK056374 Sequence
7	1218.2	91.0	2370	6	AR179441 Sequence
8	1218.2	91.0	2370	6	AX002570 Sequence
9	1218.2	91.0	2370	6	AX337834 Sequence
10	1218.2	91.0	2370	6	AX411211 Sequence
11	1218.2	91.0	2370	6	HSRNAS1PK
12	1144	85.5	2281	6	AX017284 Sequence
13	1068.6	79.9	1920	4	AF139639 Sequence
14	1015	75.9	2429	10	AF139638 Mus muscu
15	1010.2	75.5	2426	10	AF205855 Mus muscu
16	1008.6	75.4	2423	10	BC005720 Mus muscu
17	983	73.5	2435	10	RATSGPK
18	978.8	73.2	2432	6	AX056375 Sequence
19	814.8	60.9	1417	5	AF057138 Xenopus l
20	705	52.7	2470	5	SAC223715 Squalus a
21	705	52.7	3105	5	SAC223716 Squalus a
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23	533.2	39.9	2494	10	BC018363 Mus muscu
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27	527.2	39.4	1815	9	BC014037 Homo sapi
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37	481	35.9	2184	10	BC026549 Mus muscu
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39	448.6	33.5	906	10	AF361756 Rattus no
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44	283.8	21.2	2445	3	AY069856 Drosophil
45	283.8	21.2	3647	3	Z26242 D.melanog

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
AK098509
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

AK098509
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AK098509
AK098509.1 GI:21758535
oligo capping; fis (full insert sequence).
Homo sapiens stomach mucosa cDNA to mRNA, clone lib:STM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Ishibashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishida,S.,

Ono, Y., Hotuta, T., Hiraoka, S., Murakawa, K., Takiguchi, S.,
Kusano, J., Watanabe, M., Fujimori, K., Tanai, H., Ishida, M.,
Yamashita, H., Chiba, Y., Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, S.,
Morinaga, M., Kawamura, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H.,
Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and
Sugano, S.

NEDO human cDNA sequencing project

Unpublished

2 (bases 1 to 2364)

Sugano, S. and Suzuki, Y.

Direct Submission

Submitted (08-JUL-2002) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
E-mail: cdna@ims.u-tokyo.ac.jp, Tel: 81-3-5449-5286,
Fax: 81-3-5449-5416

NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction and 5'-end one pass sequencing: Institute of Medical
Science, University of Tokyo, Laboratory of Genome Structure, Human
Genome Center; 3'-end one pass sequencing: RAB; clone selection for
full insert sequencing: RAB and Helix Research Institute.

FEATURES

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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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LOCUS Homo sapiens serine/threonine protein kinase sgk mRNA, complete cds.
DEFINITION AF153609
VERSION AF153609.1 GI:5231142
KEYWORDS
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2382)
REFERENCE Kim, M.K., Kim, Y.H., Seo, J.M., Lee, H.M., Chung, H.J., Sohn, M.Y.,
AUTHORS Hwang, S.Y., Im, S.U., Jung, E.J. and Kim, J.C.
TITLE A catalogue of genes in the human dermal papilla cells as
identified by expressed sequence tags
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2382)
AUTHORS Kim, M.K., Kim, Y.H., Suh, J.M., Lee, H.M., Chung, H.J., Sohn, M.Y.,
Hwang, S.Y., Im, S.U., Jung, E.J. and Kim, J.C.
TITLE Direct Submission
JOURNAL Submitted (24-MAY-1999) Immunology, Kyungpook National University,

School of Medicine, 101 Dongin Dong, Jung Gu, Taegu, Taegu 700-422,
South Korea

FEATURES

source

Location/Qualifiers

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CDS

BASE COUNT

640 a 519 c 513 g 710 t

ORIGIN

Query Match

Best Local Similarity 91.3%; Score 1221.4; DB 9; Length 2382;

Matches 1222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY	1316	CTCCACGAGCTTTTCTCTCTGA	1338
DB	1316	CTCCACGAGCTTTTCTCTCTGA	1338

RESULT 3

BC001263

LOCUS

DEFINITION

IMAGE:3459056, mRNA, complete cds.

ACCESSION

BC001263

VERSION

BC001263.1 GI:12654838

KEYWORDS

MGC.

SOURCE

Homo sapiens.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 2382)

Strausberg R.

Direct Submission

Submitted (11-DEC-2000) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabbs-r@mail.nih.gov

Tissue procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 4 Row: a Column: 12
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 5032090.

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642 a 519 c 513 g 708 t
 BASE COUNT
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Query Match 91.3%; Score 1221.4; DB 9; Length 2382;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy	236	AGCTGAGCTTATGAATGCCAACCCCTTCTCTCCACCAAGTCTCTCAGCAATCAACC	295
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Qy	1016	GACACCTCTCTGAGGGCCCTCTGAGAGAGACAGCAAAAGCGGCTCGGGGCGCAAGATG	1075
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 DEFINITION Sequence 6 from patent US 6232077.
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 ORGANISM Unknown.
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 AUTHORS Au-Young,J., Guegler,K.J. and Hawkins,P.R.
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 JOURNAL Patent: US 6232077-A 6 15-MAY-2001;
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AK055077
ACCESSION
VERSION
KEYWORDS
SOURCE
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ORGANISM
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Nishi, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H.,
Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Ota, T., Wakamatsu, A.,
Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K.,
Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y.,
Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K.,
Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A.,
Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K.
and Isogai, T.
TITLE
JOURNAL
REFERENCE
2 (bases 1 to 3196)
AUTHORS
Isogai, T., Otsuki, T. and Sugiyama, T.
TITLE
JOURNAL
COMMENT
Submitted (24-Oct-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: RAB and
HRI.
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RESULT 6
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 AX056374
 ACCESSION
 VERSION AX056374.1 GI:12229081
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1296)
 AUTHORS Plozman,G.D., Martinez,R., Whyte,D. and Sudersanam,S.
 TITLE Protein kinases
 JOURNAL Patent: WO 0073469-A 18 07-DEC-2000;
 Sugen, Inc. (US)
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RESULT 7
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DEFINITION Sequence 1 from patent US 6326181.
ACCESSION AR179441
VERSION AR179441.1 GI:20220996
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 2370)
Lang, P. and Waldeger, S.
TITLE Cell volume-regulated human kinase h-sek
JOURNAL Patent: US 6326181-A 1 04-DEC-2001;
FEATURES Location/Qualifiers
source 1. 2370
BASE COUNT 636 a 517 c 513 g 704 t
ORIGIN

Query Match 91.0%; Score 1218.2; DB 6; Length 2370;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DEFINITION Sequence 1 from Patent EP0861896.
ACCESSION AX002570
VERSION AX002570.1 GI:7242111
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2370)
AUTHORS Lang, F.P. and Waldegger, S.D.
TITLE Cell volume regulated human kinase h-egk
JOURNAL Patent: EP 0861896-A 1 02-SEP-1998;
DADE BEHRING MARBURG GMBH (DE)
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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LOCUS Sequence 8343 from Patent WO0194629.
DEFINITION AX337834
ACCESSION AX337834
VERSION AX337834.1 GI:18128553
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
JOURNAL Patent: WO 0194629-A 8343 13-DEC-2001;
Avalon Pharmaceuticals (US)
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BASE COUNT 636 a 517 c 513 g 704 t
ORIGIN

Query Match 91.0%; Score 1218.2; DB 6; Length 2370;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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LOCUS AX411211
DEFINITION Sequence 3858 from Patent WO229103.
ACCESSION AX411211
VERSION AX411211.1 GI:21443916
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Alvares, C., Horne, D., Peres-da-Silva, S. and Vockley, J.G.
TITLE Gene expression profiles in liver cancer
JOURNAL Patent: WO 0229103-A 3858 11-APR-2002;
GENE LOGIC INC (US)
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BASE COUNT 636 a 517 c 513 g 704 t
ORIGIN

Query Match 91.0%; Score 1218.2; DB 6; Length 2370;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 116 TGGCTTTTCATGACGAGGAGGATGGGTCTGAACGACTTTATTTACAGAAATGGCCAATA 175
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DEFINITION Y10032
ACCESSION Y10032.1 GI:1834510
VERSION serine/threonine protein kinase; sgk gene.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens
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REFERENCE 1 (bases 1 to 2370)
AUTHORS Waldegger, S., Barth, P., Raber, G. and Lang, F.
TITLE Cloning and characterization of a putative human serine/threonine protein kinase transcriptionally modified during anisotonic and isotonic alterations of cell volume
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4440-4445 (1997)
MEDLINE 97272242
PUBMED 9114008
REFERENCE 2 (bases 1 to 2370)
AUTHORS Waldegger, S.

Direct Submission
Submitted (11-DEC-1996) S. Waldegger, University of Tuebingen,
Physiology I, Gmelinstr. 5, D-72076 Tuebingen, FRG
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BASE COUNT 636 a 517 c 513 g 704 t
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Query Match 91.0%; Score 1218.2; DB 9; Length 2370;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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 VERSION
 SOURCE
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 Effects on epithelial na+ channels
 J. Biol. Chem. 274 (24), 16973-16978 (1999)
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 Shigev.A., Asher.C., Latter.H., Garty.H. and Reuveny.E.
 Regulation of sgk by aldosterone and its effects on the epithelial
 Na(+) channel
 Am. J. Physiol. Renal Physiol. 278 (4), F613-F619 (2000)
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 2 (bases 1 to 2426)
 Shigev.A., Asher.C., Latter.H., Garty.H. and Reuveny.E.
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GenCore version 5.1.6
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4: sp_human:*

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6: sp_mammal:*

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9: sp_phage:*

10: sp_plant:*

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17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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11	1374.5	58.7	366	11	O8RQZ6 mus musculus
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ALIGNMENTS

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QY 97 INLGSSNNPHAKPSDFHFLKVIKGSFGKVLARHKAEEVYAVKVLQKXAILKKKEKH 156
Db 85 INLGSSNNPQAKPSDFNFKVIKGSFGKVLAKHAKDQFYAVKVLQKXAILKKKEKH 144
QY 157 IMSENRVLLKXNHKHPFLVGLHFSFQTADKLYFVLVDYINGGELFYHLQRECFLEPRARFY 216
Db 145 IMSENRVLLKXNHKHPFLVGLHFSFQTADKLYFVLVDYINGGELFYHLQRECFLEPRARFY 204
QY 217 AAEATASALGYLHSLNIVYRDLKPNILDSQGHVLTDFGLCKENIEHNSTTSTFCGTPPE 276
Db 205 AAEATASALGYLHSLNIVYRDLKPNILDSQGHVLTDFGLCKENIEHNSTTSTFCGTPPE 264
QY 277 YLAPEVLHKKQPYDRDVTDMWCLGAVLYEMLYGCLPPFYSRNTAEMVDNLNKPQLKPNITN 336
Db 265 YLAPEVLHKKQPYDRDVTDMWCLGAVLYEMLYGCLPPFYSRNTAEMVDNLNKPQLKPNISN 324
QY 337 SARHLLGLLQKORTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNPNVSGNDL 396
Db 325 SARHLLGLLQKORTKRLGAKDDFMEIKSHVFFSLINWDDLINNAKLTFFFPNPNVSGPADL 384
QY 397 RHPDPEFTEEPVPSNIGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 445
Db 385 QHPDPEFTEEPVPSNIGKSPDNLITASVKAASDAFLGFSYAPPMDSFL 433

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RESULT 4

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Q8VEK1 ID Q8VEK1 PRELIMINARY; PRT; 429 AA.
AC Q8VEK1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to serum/glucocorticoid regulated kinase-like.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018363.1; -.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR001683; PX.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR Pfam; PF00787; PX; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW Kinase.
SQ SEQUENCE 429 AA; 49077 MW; A9C6B7A0C34031F3 CRC64;

```

Query Match 63.4%; Score 1484; DB 11; Length 429;
 Best Local Similarity 68.2%; Pred. No. 2.6e-114;
 Matches 281; Conservative 53; Mismatches 70; Indels 8; Gaps 3;

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QY 41 FMKQRMGLNDFIQKIANNYSACKHPEVQSILKI-----SQQPEELMNNANSPSPSPS 94
Db 19 FIKQRRAGLNEFIQNLVRYPELYNHPDVRFLQMDSPRHQSDPSEDE-DEKSTSKPHSTS 77
QY 95 QQINLGSSNPHAKPSDFHFLKVIKGSFGKVLARHKAEEVYAVKVLQKXAILKKKEE 154

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Db 78 RNINLGPTGNPHAKPTDFDFLKVIGKSGFGKVLAKRKLKDGKYAVKVLQKXIVLNKKEQ 137
QY 155 KHIEMSENRVLLKXNHKHPFLVGLHFSFQTADKLYFVLVDYINGGELFYHLQRECFLEPRAR 214
Db 138 KHIEMSENRVLLKXNHKHPFLVGLHFSFQTTEKLYFVLDFVNGGELFFHLQRECFLEPRAR 197
QY 215 FYAAETASALGYLHSLNIVYRDLKPNILDSQGHVLTDFGLCKENIEHNSTTSTFCGT 274
Db 198 FYAAETASALGYLHSLNIVYRDLKPNILDSQGHVLTDFGLCKEGIAISDTTSTFCGT 257
QY 275 PEYLAPEVLHKKQPYDRDVTDMWCLGAVLYEMLYGCLPPFYSRNTAEMVDNLNKPQLKPN 334
Db 258 PEYLAPEVLHKKQPYDRDVTDMWCLGAVLYEMLYGCLPPFYCDVAEMVDNLNKPQLNLRPGV 317
QY 335 TNSARHLLGLLQKORTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNPNVSGPN 394
Db 318 SLTAWMSILKEELKRNQNLGAKEDFLEIQNHFFFSLSWTDLVQKKIPFPFPNPNVAGPD 377
QY 395 DLRHPDPEFTEEPVPSNIGKSPDSVLVTASVKEAAEAFGLFSYAPPT-DSFL 445
Db 378 DIRNFDVFEETETVPYSCVSSDYSIVNASVLEADDAFVGFSYAPPSDELFL 429

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RESULT 5

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Q9ERE3 ID Q9ERE3 PRELIMINARY; PRT; 496 AA.
AC Q9ERE3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Serine/threonine protein kinase CISK.
DE CISK.
GN CISK.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20504817; PubMed=11050396;
RA Liu D., Yang X., Songyang Z.;
RT "Identification of CISK, a new member of the SGK kinase family that
RL Curr. Biol. 10:1233-1236(2000).
RL EMBL; AF312007; AAG34115.1; -.
DR HSSP; P05132; IATP.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR001683; PX.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR Pfam; PF00787; PX; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00312; PX; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 496 AA; 57145 MW; 4B7D2804A5948BAD CRC64;

```

Query Match 63.4%; Score 1484; DB 11; Length 496;
 Best Local Similarity 68.2%; Pred. No. 3.2e-114;
 Matches 281; Conservative 53; Mismatches 70; Indels 8; Gaps 3;

```

QY 41 FMKQRMGLNDFIQKIANNYSACKHPEVQSILKI-----SQQPEELMNNANSPSPSPS 94
Db 86 FIKQRRAGLNEFIQNLVRYPELYNHPDVRFLQMDSPRHQSDPSEDE-DEKSTSKPHSTS 144
QY 95 QQINLGSSNPHAKPSDFHFLKVIKGSFGKVLARHKAEEVYAVKVLQKXAILKKKEE 154

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Db 145 RNINLPGTGNPHAKPTDFELKVGSGFKVLLAKRKLKDGKFAVAVKVLQKTVLNKQ 204
Qy 155 KHIMSENVLLKNVHPFLVGLHFSFOTADKLYFVLDYINGGELFVHLQRCFLPRAR 214
Db 205 KHMAERNVLLKNVHPFLVGLHFSFOTTEKLYFVLDYFVNGGELFVHLQRCFLPRAR 264
Qy 215 FYAAEIASALGYLHSLNIVYRDLPENILLDSOGHIVLTDGFLCKENIEHNSTTFCGT 274
Db 265 FYAAEIASALGYLHSLNIVYRDLPENILLDSOGHIVLTDGFLCKENIEHNSTTFCGT 324
Qy 275 PEYLAPEVLHQPVDRTVDMWCLGAVLYEMLYGLPPFYSNTAEYDNLINKLPQLKPN 334
Db 325 PEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYSNTAEYDNLINKLPQLKPN 384
Qy 335 TNSARHLLLEGLOKDKRTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNVSGPN 394
Db 385 SLTAWMSILEELKQNRNLGAKEDFLEIQNHFFESLSWTDLVQKKIPPPFPNVAGPD 444
Qy 395 DLRFHDFEETPEEPVNSIGKSPSVLVTASVKAABAFGLFSYAPPT-DSFL 445
Db 445 DIRNFDAVTEETVPYSCVSSDYSIVNASVLEADDAFVGSYAPPSDELFL 496

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RESULT 6

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Q96BR1 ID Q96BR1 PRELIMINARY; PRT; 496 AA.
AC Q96BR1; Q9UGS;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 57.1 kDa protein (Protein kinase).
GN SGK3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1.
RP SEQUENCE FROM N.A.
RC TISSUE=BRST;
RA Strauberg R.;
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
[2]
RN 2.
RP SEQUENCE OF 68-496 FROM N.A.
RX MEDLINE=20018032; PubMed=10548550;
RX Kobayashi T., Deak M., Morrice N., Cohen P.;
RT "Characterization of the structure and regulation of two novel
RT isoforms of serum- and glucocorticoid-induced protein kinase.";
RL Biochem. J. 344:189-197(1999).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; BC015326; AAL15326.1; -.
DR EMBL; AF169035; AAF12758.1; -.
DR HSP; P05132; IATP.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR001683; PX.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR Pfam; PF00787; PX; 1.
DR ProDom; PD000001; Euk_pkinase; 1..
DR SMART; SMO0133; S_TK_X; 1.
DR SMART; SMO0133; S_TK_X; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW Hypothetical protein; ATP-binding; Kinase;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 496 AA; 57108 MW; 76A6CCEB69006CFL CRC64;

```

Query Match 63.1%; Score 1476; DB 4; Length 496;
 Best Local Similarity 67.5%; Pred. No. 1.5e-113;
 Matches 280; Conservative 52; Mismatches 69; Indels 14; Gaps 3;

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Qy 41 FMKQRMGLNDFQTKIANNYSACKHPEVOSILKIQEPPELMNANPSPPP 91
Db 86 FIKQRRAGLNEFQNLVRYPELYNHPDVRAFLQMDSPKH----QSDPSEDESSQKLH 141
Qy 92 SPSQINLGPSGNPHAKPTDFELKVGSGFKVLLAKRKLKDGKFAVAVKVLQKTVLN 151
Db 142 STSQINLGPSGNPHAKPTDFELKVGSGFKVLLAKRKLKDGKFAVAVKVLQKTVLN 201
Qy 152 KEEKHIMSENVLLKNVHPFLVGLHFSFOTADKLYFVLDYINGGELFVHLQRCFLPR 211
Db 202 KEQKHIMSENVLLKNVHPFLVGLHFSFOTTEKLYFVLDYFVNGGELFVHLQRCFLPR 261
Qy 212 RARFYAAEIASALGYLHSLNIVYRDLPENILLDSOGHIVLTDGFLCKENIEHNSTT 271
Db 262 RARFYAAEIASALGYLHSLNIVYRDLPENILLDSOGHIVLTDGFLCKENIEHNSTT 321
Qy 272 CGTPEYLAPEVLHQPVDRTVDMWCLGAVLYEMLYGLPPFYSNTAEYDNLINKLPQL 331
Db 322 CGTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYSNTAEYDNLINKLP 381
Qy 332 PNITNSARHLLLEGLOKDKRTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPP 391
Db 382 PGVSLTAWMSILEELKQNRNLGAKEDFLEIQNHFFESLSWADLVQKKIPPPFPNV 441
Qy 392 GPNDLRHDFEETPEEPVNSIGKSPSVLVTASVKAABAFGLFSYAPPT-DSFL 445
Db 442 GPDDIRNFDAVTEETVPYSCVSSDYSIVNASVLEADDAFVGSYAPPSDELFL 496

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RESULT 7

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Q9PLQ7 ID Q9PLQ7 PRELIMINARY; PRT; 496 AA.
AC Q9PLQ7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE SGK-like protein SGK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1.
RP SEQUENCE FROM N.A.
RX MEDLINE=20054360; PubMed=10585774;
RX Dai F., Yu L., He H., Zhao Y., Yang J., Zhang X., Zhao S.;
RT "Cloning and mapping of a novel human Serum/Glucocorticoid regulated
RT kinase-like gene, SGK, to chromosome 8q12.3-q13.1.";
RL Genomics 62:95-97(1999).
RN 2.
RP SEQUENCE FROM N.A.
RA Zhao Y.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF085233; AAF27051.2; -.
RX HSP; P05132; IATP.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR001683; PX.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR Pfam; PF00787; PX; 1.
DR ProDom; PD000001; Euk_pkinase; 2.
DR SMART; SMO0132; PX; 1.
DR SMART; SMO0220; S_TK_X; 1.
DR SMART; SMO0133; S_TK_X; 1.
DR SMART; SMO0219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
SQ SEQUENCE 496 AA; 56995 MW; DAAEA2E736C90822C CRC64;

```

Query Match 62.5%; Score 1463; DB 4; Length 496;
Best Local Similarity 67.0%; Pred. No. 1.8e-112;
Matches 278; Conservative 51; Mismatches 72; Indels 14; Gaps 3;

QY 41 FMKORRLNDFIQKIANNSVACHPEVQSILKISQPOEPELMANSPSP-----91
DB 86 FIKORRLNDFIQKIANNSVACHPEVQSILKISQPOEPELMANSPSP-----91
QY 92 SPSQOINLPGSNPHAKPSDFHFLKVGKSGFGLLAKHAEVYAVKVLQKAILKK 151
DB 142 STSQINLPGSNPHAKPSDFHFLKVGKSGFGLLAKHAEVYAVKVLQKAILKK 201
QY 152 KEEKHINSENVLLKVKHPELVGLHFSFQADKLYFLVDYINGGELFYHLQRCLEP 211
DB 202 KEQKHIAERNVLLKVKHPELVGLHFSFQADKLYFLVDYINGGELFYHLQRCLEP 261
QY 212 RARFYAAEIASALGYLSNIVYDLKPENILDSOGHIVLTDGLCKENIEHNSSTSF 271
DB 262 RARFYAAEIASALGYLSNIVYDLKPENILDSOGHIVLTDGLCKENIEHNSSTSF 321
QY 272 CGTEYLAPEVLHAKOPDRTVDWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKLQK 331
DB 322 CGTEYLAPEVLHAKOPDRTVDWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKLQK 381
QY 332 PNITNSARHLLEGILQKDRTRKLGAKODFMEIKSHVFFSLINWDDLKNTTPPNVNS 391
DB 382 PGVSLRAWSILEEULEKDRNLQKAKEDFLEIQNHPPFESISWADLVQKKIPPPFNVA 441
QY 392 GPNDLRHFDPEETPEEPNSIGKSPDSVLVTASVKEAAEALGFSYAPPT-DSFL 445
DB 442 GPNDLRHFDPEETPEEPNSIGKSPDSVLVTASVKEAAEALGFSYAPPT-DSFL 496

RESULT 8
Q9HBY8 PRELIMINARY; PRT; 427 AA.
AC Q9HBY8
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Protein kinase.
GN SGK2BETA
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20018032; PubMed=10548550;
RA Kobayashi T., Deak M., Morrice N., Cohen P.;
RT "Characterization of the structure and regulation of two novel
RT isoforms of serum- and glucocorticoid-induced protein kinase.";
RL Biochem. J. 344:189-197(1999).
DR EMBL; AF186470; AAG17012.1; -.
DR HSSP; P05132; IATP.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase C; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00133; S_TK X; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Transferase
SQ SEQUENCE 427 AA; 47604 MW; D8F0FA6DF54B1370 CRC64;

Query Match

60.6%; Score 1419; DB 4; Length 427;

Best Local Similarity 68.3%; Pred. No. 6.2e-109;
Matches 267; Conservative 56; Mismatches 54; Indels 14; Gaps 4;

QY 66 PEVQSILKISQPOEPEL-----MNANP---SPSPSQ---QINLPGSNPHAKPSDFH 114
DB 38 PPTPTLSCLLLPVPPELPDHCYRMNSSPAGTSPQPSRANGNINLGSANPNAQPTDFDP 97
QY 115 LKVGKSGFGLLAKHAEVYAVKVLQKAILKKKEKHIMSENVLLKVKHPELV 174
DB 98 LKVGKSGFGLLAKHAEVYAVKVLQKAILKKKEKHIMSENVLLKVKHPELV 157
QY 175 GLHFSFQADKLYFLVDYINGGELFYHLQRCLEPFRARFYAAEIASALGYLSNIVY 234
DB 158 GLHFSFQADKLYFLVDYINGGELFYHLQRCLEPFRARFYAAEIASALGYLSNIVY 217
QY 235 RDLKPENILDSOGHIVLTDGLCKENIEHNSSTSFCTGTPPEVLAPVLHAKOPDRTVDW 294
DB 218 RDLKPENILDSOGHIVLTDGLCKENIEHNSSTSFCTGTPPEVLAPVLHAKOPDRTVDW 277
QY 295 WCLGAVLYEMLYGLPPFYSRNTAEMYNILNKLQKPNITNSARHLLEGILQKDRTRK 354
DB 278 WCLGAVLYEMLYGLPPFYSRNTAEMYNILNKLQKPNITNSARHLLEGILQKDRTRK 337
QY 355 GAKODFMEIKSHVFFSLINWDDLKNTTPPNVNSIGKSPDSVLVTASVKEAAEALGFSYAPPT-DSFL 445
DB 338 GSKADFLKIEIKHNVFFSPINWDDLKNTTPPNVNSIGKSPDSVLVTASVKEAAEALGFSYAPPT-DSFL 445
QY 415 SPDSVLVTASVKEAAEALGFSYAPPT-DSFL 445
DB 398 TPDTV---ASSGASSAFLGFSYAPEDDDIL 425

RESULT 9

Q9UKG6 PRELIMINARY; PRT; 367 AA.
AC Q9UKG6
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Protein kinase (DJI1387.2) (Serum/glucocorticoid regulated kinase 2)
DE (Similar to serum/glucocorticoid regulated kinase 2).
GN SGK2ALPHA OR SGK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20018032; PubMed=10548550;
RA Kobayashi T., Deak M., Morrice N., Cohen P.;
RT "Characterization of the structure and regulation of two novel
RT isoforms of serum- and glucocorticoid-induced protein kinase.";
RL Biochem. J. 344:189-197(1999).
DR EMBL; AF186470; AAG17012.1; -.
DR HSSP; P05132; IATP.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase C; 1.

```

DR PRINTS; PR00109; TYRKINASE.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TK_X; 1.
DR SMART; SM00220; S_TK_X; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 367 AA; 41174 MW; E53FIABE253F649B CRC64;

Query Match          60.3%; Score 1411; DB 4; Length 367;
Best Local Similarity 71.2%; Pred. No. 2.3e-108;
Matches 262; Conservative 53; Mismatches 45; Indels 8; Gaps 3;

QY 83 MNANP--SPPPSPSQ---QINLGSSNPHAKPSDFHLKVIKGSFGKVLARHKAEEVF 137
DB 1 MNSSPAGTSPQPSRANGNINLGSAFNAPQPTDFDLKVIKGNKGVLLAKRSDGAF 60
QY 138 YAVVLQKAILKKKEKHIMSERVLLKNVHFPFLVGLHFSFOTADKLYFVLDYINGGE 197
DB 61 YAVVLQKSKLKKKEKHIMSERVLLKNVHFPFLVGLHFSFOTADKLYFVLDYINGGE 120
QY 198 LFYHLQRCFLPRARFYAAEIASALGYLHSLNIVYRDLPENILLDSQGHIVLTDPL 257
DB 121 LFFHLQRRERFLPRARFYAAEIASALGYLHSLNIVYRDLPENILLDSQGHIVLTDPL 180
QY 258 CKENIEHNTSTSTCGTPEYLAPEVLHQPVDRTVDMWCLGAVLYEMLYGLPPYSNTA 317
DB 181 CKGEVEPEDTSTCGTPEYLAPEVLHQPVDRTVDMWCLGAVLYEMLYGLPPYSQDVS 240
QY 318 EYONILNKLQPKNTNSARHLLGLLQKDRKLGAKDDFMEIKSHVFFSLINWDDL 377
DB 241 QYENILHQPLOIPGGRTVAACDLQLSLHDKQRLGSKADFLKIKHVVFFSPINWDDL 300
QY 378 INKKTTPFPNVSQPNLDRHDFEFTPEEPVNSIGKSPSVLVTASVKEAAEAFGLFSY 437
DB 301 YHKELTPFPNVTGPADLKHDFEFTQEA VSKSIGCTPTDV---ASSSGASSAFLGFSY 357

QY 438 APPTDSFL 445
DB 358 APEDDDIL 365

RESULT 10
Q9QZ55 ID Q9QZ55 PRELIMINARY; PRT; 367 AA.
AC Q9QZ55;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Protein kinase.
GN SGK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20018032; PubMed=10548550;
RA Kobayashi T., Deak M., Morrice N., Cohen P.;
RT "Characterization of the structure and regulation of two novel
RT isoforms of serum- and glucocorticoid-induced protein kinase.";
RL Biochem. J. 344:189-197(1999).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF169033; AAF12756.1; -.
DR HSSP; P05132; 1CTP.
DR MGD; MGI:1351318; SGK2.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR ProDom; PD000001; Euk_pkinase; 1.

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DR SMART; SM00220; S_TK_X; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 367 AA; 41359 MW; 668C04B1A1E9E33A CRC64;

Query Match          59.3%; Score 1387; DB 11; Length 367;
Best Local Similarity 71.1%; Pred. No. 2.2e-106;
Matches 256; Conservative 51; Mismatches 49; Indels 4; Gaps 2;

QY 87 PSPPPSPSQ-QINLGSSNPHAKPSDFHLKVIKGSFGKVLARHKAEEVFYAVKVLQK 145
DB 9 PSPQPSRANGNINLGSAFNAPQPTDFDLKVIKGNKGVLLAKRSDGAFYAVKVLQK 68
QY 146 KAILKKKEKHIMSERVLLKNVHFPFLVGLHFSFOTADKLYFVLDYINGGEYFHLQRE 205
DB 69 KSLKKNKEQHIMAEARNVLLKNVHFPFLVGLHFSFOTADKLYFVLDYINGGEYFHLQRE 128
QY 206 RCFLPRARFYAAEIASALGYLHSLNIVYRDLPENILLDSQGHIVLTDPLCKENIEHN 265
DB 129 RRELEPRARFYAAEIASALGYLHSLNIVYRDLPENILLDSQGHIVLTDPLCKECVEPE 188
QY 266 STTSTFCGTPEYLAPEVLHQPVDRTVDMWCLGAVLYEMLYGLPPYSNTASYDNILN 325
DB 189 EYTSTFCGTPEYLAPEVLHQPVDRTVDMWCLGAVLYEMLYGLPPFNTDVAQMYENILH 248
QY 326 KPIQLKPNITNSARHLLGLLQKDRKLGAKDDFMEIKSHVFFSLINWDDLINKKITPP 385
DB 249 QPLQIPGRTVAACDLQLSLHDKQRLGSKEDFLDKNHMFSPINWDDLHYKRLTTP 308
QY 386 FNPVNSQPNLDRHDFEFTPEEPVNSIGKSPSVLVTASVKEAAEAFGLFSYAPPTDSFL 445
DB 309 FNPVNSQPNLDRHDFEFTPEEPVNSIGKSPSVLVTASVKEAAEAFGLFSYAQDDDDIL 365

RESULT 11
Q8ROP6 ID Q8ROP6 PRELIMINARY; PRT; 366 AA.
AC Q8ROP6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Serum/glucocorticoid regulated kinase 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026549; AAH26549.1; -.
KW Kinase.
SQ SEQUENCE 366 AA; 41231 MW; D6786996069EF3F4 CRC64;

Query Match          58.7%; Score 1374.5; DB 11; Length 366;
Best Local Similarity 71.1%; Pred. No. 2.4e-105;
Matches 256; Conservative 50; Mismatches 49; Indels 5; Gaps 3;

QY 87 PSPPPSPSQ-QINLGSSNPHAKPSDFHLKVIKGSFGKVLARHKAEEVFYAVKVLQK 145
DB 9 PSPQPSRANGNINLGSAFNAPQPTDFDLKVIKGNKGVLLAKRSDGAFYAVKVLQK 68
QY 146 KAILKKKEKHIMSERVLLKNVHFPFLVGLHFSFOTADKLYFVLDYINGGEYFHLQRE 205
DB 69 KSLKKNKEQHIMAEARNVLLKNVHFPFLVGLHFSFOTADKLYFVLDYINGGEYFHLQRE 127
QY 206 RCFLPRARFYAAEIASALGYLHSLNIVYRDLPENILLDSQGHIVLTDPLCKENIEHN 265
DB 128 RRELEPRARFYAAEIASALGYLHSLNIVYRDLPENILLDSQGHIVLTDPLCKECVEPE 187

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QY 266 STTSTFCGTEYLAEVHLKQYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLN 325
 DB 188 ETTSTFCGTEYLAEVHLKQYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLN 247
 QY 326 KPLQKRNNTSARHLLGLLQKQRTKRLGAKDDFMEIKSHVFSNLNWDLLINKKITPP 385
 DB 248 QPLQIPGRTVAACDLQLGGLHDKQRLGSKEDFLDKNHMFSPINWDDLHYKRLTTP 307
 QY 386 FPNVSGPDLRHFDPTEEPVNSIGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 445
 DB 308 FPNVEGPADLKHDFDEFTQEAQVSKSGCTPDIV--ASSSGASSAFGLFSYAQDDDL 364

RESULT 12
 Q8R4U9 ID Q8R4U9 PRELIMINARY; PRT; 302 AA.
 AC Q8R4U9
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Serum- and glucocorticoid-inducible kinase 2-related (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN RN
 RC SEQUENCE FROM N.A.
 RP STRAIN=SPRAGUE-DAWLEY; TISSUE=KIDNEY;
 RA Feng Y.X., Huber S.M., Waerniges S., Lang F.;
 RT "SGK2 and SGK3 mRNA expression in rat kidney."
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF361756; AAL91351.1;
 KW Kinase.
 FT NON_TER 1 1
 FT NON_TER 302 302
 SQ SEQUENCE 302 AA; 34622 MW; A74BE3F424283D66 CRC64;

Query Match 52.8%; Score 1236; DB 11; Length 302;
 Best Local Similarity 74.0%; Pred. No. 5.1e-94;
 Matches 222; Conservative 45; Mismatches 33; Indels 0; Gaps 0;

QY 97 INLPSNPHAKPSDFHLKVIKSGFGKVLARHKAEEVYAVKQLKKEKH 156
 DB 3 INLPSANPNARPTDFDLKVIKSGNYGVLLAKRSDGAFYAVKQLKKEQSH 62
 QY 157 IMSENVLLKNVHPLVGLHFSFQADKLYFVLDYINGGELFYHLORECFLEPRFY 216
 DB 63 IMAEVLLKNVRHPLVGLHFSFQADKLYFVLDYINGGELFYHLORECFLEPRFY 122
 QY 217 AABIASALGYLHSLNIVYRDLKPNILLDSQGHVLTDFGLCKENIEHNSTTSTFCGTP 276
 DB 123 TAEVASAIGYLSLNIYRDLKPNILLDCQGHVLTDFGLCKEVEPEETSTFCGTP 192
 QY 277 YLAPEVHLKQYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLNPLQKNITN 336
 DB 183 YLAPEVHLKQYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLNPLQIPGRTV 242
 QY 337 SARHLLGLLQKQRTKRLGAKDDFMEIKSHVFSNLNWDLLINKKITPPNPNVSGNDL 396
 DB 243 AACDLQGLLHDKQRLGSKEDFLDKNHMFSPINWDDLHYKRLTTPPNVSGPADL 302

RESULT 13
 Q94365 ID Q94365 PRELIMINARY; PRT; 422 AA.
 AC Q94365
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE W10G6.2 protein.
 DE W10G6.2.
 OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN RN
 RP SEQUENCE FROM N.A.
 RA McMurray A.A.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology."
 RL Science 282:2012-2018(1998).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; Z81140; CAB03485.1;
 DR HSSP; P05132; IATP.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00433; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00133; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE-ST; 1.
 DR ATP-binding; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 422 AA; 49672 MW; 1FA5EF677B88C00 CRC64;

Query Match 46.2%; Score 1082; DB 5; Length 422;
 Best Local Similarity 52.0%; Pred. No. 4.3e-91;
 Matches 204; Conservative 71; Mismatches 99; Indels 18; Gaps 4;

QY 32 ESFLLSGLAPMKQRMGLNDFQKIANNYSACKHPVEQVSIKISQOEPELMANPSPPP 91
 DB 29 KKFLQADSKFYEKRRVWILVISQHLVDNN--LRSEDEVRRFFHLESPPDDDE----- 76
 QY 92 SPSQQLNLGPNSSNPHAKPSDFHLKVIKSGFGKVLARHKAEEVYAVKQLKKEKH 151
 DB 77 ---NNVDLSPERKATANDFDYLTITIGKSGFRVYQVRHKTCKIYAMKILSKHIRKK 133
 QY 152 KEEKIMTSERNVLLKNVHPLVGLHFSFQADKLYFVLDYINGGELFYHLORECFLEP 211
 DB 134 NEVKHVAERNVLLNFKHPLVGLHFSFQADKLYFVLDHNGELFYHLORECFHSES 193
 QY 212 RARFYAAETASALGYLHSLNIVYRDLKPNILLDSQGHVLTDFGLCKENIEHNSTTSTF 271
 DB 194 RSRFYAAETACALGYLHSLNIVYRDLKPNILLDDKGYLVTDFGLCKEDMQSKTTSTF 253
 QY 272 CGTPEYLAPEVHLKQYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLNPLQK 331
 DB 254 CGTPEYLAPEVHLKQYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLNPLQK 313
 QY 332 PNITNSARHLLGLLQKQRTKRLGAKDDFMEIKSHVFSNLNWDLLINKKITPPNPNVS 391
 DB 314 HNISVPCSELTGLLQKQSKRLGHRNDFRDRHPPFLVPDWDKLLNRELKAPFPKVK 373
 QY 392 GNDLURHFDPTEEPV--PNSIGKSPDSVLVT 422
 DB 374 NAMDTSNISKEFVEIQIDPSSL--APQLAVT 403

RESULT 14
 Q99LU4 ID Q99LU4 PRELIMINARY; PRT; 185 AA.
 AC Q99LU4
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Similar to serum/glucocorticoid regulated kinase (fragment).
 GN SGK.

OS Mus musculus (Mouse).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR ENBL; BC002222; AH02222.1; -
 DR MGD; MGI:134062; Sgk.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000961; Kinase C.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR pfam; PF00069; pkinase; 1.
 DR pfam; PF00433; pkinase; C; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR SMART; SM00133; S_TK X; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Kinase.
 FT NON_TER
 SQ SEQUENCE 185 AA; 20921 MW; EDAA44ABF083945 CRC64;
 Query Match 40.6%; Score 951; DB 11; Length 185;
 Best Local Similarity 96.1%; Pred. No. 9.3e-71;
 Matches 174; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 265 NNTSTFCGTPPEYLAPEVLHQPYDRTVDMWCLGAVLYEMLYGLPPFYGRNTAEMVDNII 324
 Db 5 NGTSTFCGTPPEYLAPEVLHQPYDRTVDMWCLGAVLYEMLYGLPPFYGRNTAEMVDNII 64
 QY 325 NKPLQKPNITNSARHLLEGLOKDRTRIGAKDFMEIKSHVFFSLINWDDLINKKITP 384
 Db 65 NKPLQKPNITNSARHLLEGLOKDRTRIGAKDFMEIKSHVFFSLINWDDLINKKITP 124
 QY 385 PFNPVNSGPNDLRHFDPEFTTEEPVNSIGKSPDSVLVTASVKEAAEAFGLGFSYAPPTDSF 444
 Db 125 PFNPVNSGPNDLRHFDPEFTTEEPVNSIGKSPDSVLVTASVKEAAEAFGLGFSYAPPTDSF 184
 QY 445 L 445
 Db 185 L 185
 RESULT 15
 Q96QV3 PRELIMINARY; PRT; 465 AA.
 AC Q96QV3;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Protein Kinase B gamma 1.
 GN AKT3.
 OS Homo sapiens (Human).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=11387345;
 RA Brodbeck D., Hill M.M., Hemmings B.A.;
 RT "Two Splice Variants of Protein Kinase B gamma Have Different
 RT Regulatory Capacity Depending on the Presence or Absence of the
 RT Regulatory Phosphorylation Site Serine 472 in the Carboxyl-terminal
 RT Hydrophobic Domain."
 RL J. Biol. Chem. 276:29550-29558(2001).
 DR ENBL; AY005799; AAF91073.1; -
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR000961; Kinase C.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR * pfam; PF00169; PH; 1.

DR pfam; PF00069; pkinase; 1.
 DR pfam; PF00433; pkinase; C; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00219; TyrKC; 1.
 DR PROSITE; PS50003; PH DOMAIN; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
 KW ATP-binding; Kinase; Transferase.
 SQ SEQUENCE 465 AA; 54032 MW; 592EF8B86937D1E0 CRC64;
 Query Match 39.0%; Score 912; DB 4; Length 465;
 Best Local Similarity 47.0%; Pred. No. 5.4e-67;
 Matches 167; Conservative 63; Mismatches 120; Indels 28; Gaps 7;
 QY 33 SFLLSGLAFMKORRMGLNDFIOK-----IANNSTACKHPE-----VQSILKISQSQ 78
 Db 53 NFSVAKCQLMKTERPKPNTFIIRCLQWTTVIERTFHVDTPEEREWEATEIAQVADRLQR 112
 QY 79 EPELMANPSPPPSPSQINLG---PSSNPHAK---PSDFHLKLVIGKSGFKVLLARH 131
 Db 113 EERMNCSPT-----SQDNI GEEEMDASTTHHKRTMDFDYLKLLGKGTGKVLVRE 167
 QY 132 KAEVEFYAVKVLQKAILKKKEEKHIMSERNVLLKNVHPFLVGLHFSFQTADKLYFVLD 191
 Db 168 KASGKYAMKILKKEVIIAKDEVAHTLTESRV-LKNTRHPFLTSLKYSFQTKDRLCFVME 226
 QY 192 YINGGELFVHLORECFLEPRARFYAAETASALGYLHSLNIVYRDLPENILLDSOGHIV 251
 Db 227 YVNGGELFPHLSRERVFSEDRTRFYCAEIVSALDYLSHGKIYVRDLKLENMLDKDGHK 286
 QY 252 LTDFGLCKENIEHNSTSTFCGTPEYLAPEVLHQPYDRTVDMWCLGAVLYEMLYGLPPF 311
 Db 287 ITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDDNDYGRAVDWGLGVVYENWCGRLPF 346
 QY 312 YGRNTAEMVDNIIKPLQLKPNITNSARHLLEGLOKDRTRIGAKDFMEIKSHVFFS 370
 Db 347 YNQDHEKLPFLIMEDIKFPRTLSSDAKSLLSGLLIKDPNKLGGGPDDAKEIMRHSFFS 406
 QY 371 LINWDDLINKKITPPFPNPVNSGPNDLRHFDPEFTTEEPV 408
 Db 407 GVNWDQVDYDKLVPPFPKQVTSSETDTRYPDEEFTAQTI 444
 Search completed: June 20, 2003, 19:26:46
 Job time : 85 secs

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OM protein - protein search, using sw model

Run on: June 20, 2003, 19:15:08 ; Search time 22 Seconds
(without alignments)
838.953 Million cell updates/sec

Title: US-10-067-977-2

Perfect score: 2340

Sequence: 1 MGENQALARLESLLRPR.....KEAAEFLGFSYAPPTDSDL 445

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2150	91.9	431	1	SGK_HUMAN
2	2111	90.2	431	1	SGK_RABIT
3	2107	90.0	431	1	SGK_MOUSE
4	2100.5	89.8	430	1	SGK_RAT
5	916	39.1	479	1	AKT3_HUMAN
6	916	39.1	479	1	AKT3_MOUSE
7	910	38.9	454	1	AKT3_RAT
8	878	37.5	480	1	KRAC_RAT
9	878	37.5	501	1	KAKT_MLVAT
10	876	37.4	480	1	KRAC_MOUSE
11	864.5	36.9	479	1	PK2_DICDI
12	863.5	36.9	481	1	AKT2_HUMAN
13	862	36.8	480	1	KRAC_BOVIN
14	861.5	36.8	481	1	AKT2_MOUSE
15	861	36.8	480	1	KRAC_HUMAN
16	857	36.6	444	1	KRAC_DICDI
17	852.5	36.4	481	1	AKT2_RAT
18	831.5	35.5	677	1	YPK2_YEAST
19	827.5	35.4	680	1	YPK1_YEAST
20	816	34.9	485	1	K6B2_MOUSE
21	810.5	34.6	482	1	K6B2_HUMAN
22	807	34.5	502	1	K6B1_HUMAN
23	807	34.5	502	1	K6B1_RAT
24	799	34.1	634	1	KPC3_DROME
25	796.5	34.0	1016	1	PKC2_SCHPO
26	791.5	33.8	672	1	KPCA_HUMAN
27	791.5	33.8	672	1	KPCA_RAT
28	791.5	33.8	743	1	KPC2_APLCA
29	790.5	33.8	672	1	KPCA_RABIT
30	789.5	33.7	672	1	KPCA_BOVIN
31	784.5	33.5	649	1	KPC1_APLCA
32	784	33.5	671	1	KPCB_HUMAN
33	783	33.5	671	1	KPCB_MOUSE

34 783 33.5 671 1 KPCB_RABIT P05772 oryctolagus
35 781 33.4 707 1 KPCA_MOUSE P34885 caenorhabdi
36 780.5 33.4 672 1 KPCA_MOUSE P20444 mus musculu
37 779.5 33.3 988 1 PKC1_SCHPO P36582 schizosacch
38 778.5 33.3 737 1 KPCF_MOUSE P16054 mus musculu
39 776 33.2 696 1 SKC1_SCHPO P50530 schizosacch
40 776 33.2 737 1 KPCF_HUMAN Q02156 homo sapien
41 774.5 33.1 587 1 KPCI_HUMAN P41743 homo sapien
42 772.5 33.0 586 1 KPCI_MOUSE Q62074 mus musculu
43 772.5 33.0 736 1 KPCF_RABIT P10830 oryctolagus
44 767 32.8 682 1 KPCG_BOVIN P05128 bos taurus
45 765 32.7 658 1 KPCI_LYPTI Q25378 lytechinus

ALIGNMENTS

RESULT 1
ID SGK_HUMAN STANDARD; PRT; 431 AA.
AC O00141; Q9UN56;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase Sgk (EC 2.7.1.-)
DE (Serum/glucocorticoid-regulated kinase).
GN SGK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=97272242; PubMed=91144008;
RX Waldegger S., Barth P., Raber G., Lang F.;
RT "Cloning and characterization of a putative human serine/threonine
RT protein kinase transcriptionally modified during anisotonic and
RT isotonic alterations of cell volume."
RL Proc. Natl. Acad. Sci. U.S.A. 94:4440-4445(1997).
RN [2]
RP SEQUENCE FROM N.A.
MEDLINE=98390195; PubMed=9722955;
RA Waldegger S., Erdel M., Nagl U.O., Barth P., Raber G., Steuer S.,
RA Utermann G., Paulmichl M., Lang F.;
RT "Genomic organization and chromosomal localization of the human SGK
RT protein kinase gene."
RL Genomics 51:299-302(1998).
RN [3]
RP SEQUENCE FROM N.A.
Kim M.K., Kim Y.H., Seo J.M., Lee H.M., Chung H.J., Sohn M.Y.,
Hwang S.Y., Im S.U., Jung E.J., Kim J.C.;
RA "A catalogue of genes in the human dermal papilla cells as identified
RT by expressed sequence tags."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
TISSUE=Cervix;
RA Strausberg R.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROBABLE PROTEIN KINASE THAT MAY ACT IN RENAL EPITHELIA
CC TO ACTIVATE APICAL SODIUM CHANNELS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y10032; CAA71138.1; -;
DR EMBL; AJ000512; CAA04146.1; -;

	Query Match	90.08;	Score 2107;	DB 1;	Length 431;
	Best Local Similarity	93.08;	Pred. No. 3.7e-140;		
	Matches 398;	Conservative	12;	Mismatches 12;	Indels 6; Gaps 1;
Qy	24	RRAQAQ-----RSEFLLSGLAPMKORRMGLNDFIOKIANNYSYACKHPEVQSILKISQ	77		
Db	4	KABAASTLTYSRMRGVAVILIAFMKORRMGLNDFIOKIASNTYACKHAEVQSILKMSHP	63		

EMBL; AL117525; CAB55977.1; ALT_TERM.
DR HSP; P05132; IFMO.
DR Gnew; HGNC:393; AKT3.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00433; pkinase C; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Euk_pkinase; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00003; PH_DOMAIN; 1.
DR Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Alternative splicing.
FT DOMAIN 5 107 PH.
FT NP_BIND 148 405 PROTEIN KINASE.
FT BINDING 154 162 ATP (BY SIMILARITY).
FT ACT_SITE 177 177 ATP (BY SIMILARITY).
FT MOD_RES 271 271 BY SIMILARITY.
FT MOD_RES 305 305 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 472 472 PHOSPHORYLATION (BY SIMILARITY).
FT VARSPIC 452 479 YDEGDCMNERARPPQPSYASGRE -> CQSDCGML
FT MUTAGEN 305 305 T-A: NO ACTIVATION AFTER PERNADATE
TREATMENT.
FT MUTAGEN 305 305 T-D: 2 FOLD INCREASE OF PHOSPHORYLATION
STEADY STATE LEVEL, NO ACTIVATION AFTER
PERVANADATE TREATMENT.
FT MUTAGEN 447 447 T-A: NO EFFECT.
FT MUTAGEN 447 447 T-D: NO EFFECT.
FT MUTAGEN 472 472 S-A: 67% DECREASE OF ACTIVITY AFTER
PERVANADATE TREATMENT.
FT MUTAGEN 472 472 S-D: 1.4 FOLD INCREASE OF
PHOSPHORYLATION STEADY STATE LEVEL, 50%
DECREASE OF ACTIVITY AFTER PERNADATE
TREATMENT.
SQ SEQUENCE 479 AA; 55774 MW; F08BDE6502E78FB CRC64;

Query Match 39.1%; Score 916; DB 1; Length 479;
Best Local Similarity 45.1%; Pred. No. 7e-57;
Matches 193; Conservative 67; Mismatches 140; Indels 28; Gaps 7;

QY 33 SFLSLGLAFMKQRMGLNDFIQK-----IANNYSACKHPE-----VQSILKISQPO 78
DB 53 NFSVAKCOLMKTREPKNTEFIICLQWTVIERTFHVDTPEEREWEATEIQAVADRLQRO 112
QY 79 EPELMANAPPPSPSQINLG----PSSNPHAK---PSDFHLKVIKGSFGKVLARH 131
DB 113 EEREMNCSP-----SQIDNIGEEEMDASTTHKRKTMDFDVLLKLGKGTFGKVLVRE 167
QY 132 KAEVFYAVKVLQKALKKEEKHIMSERVLLKNVHPFLVGLHPSFOTADKLFLVD 191
DB 168 KASGKYVAKILKEVIAKDEVAHTLTESRV-LKNTRHPFLTSLKYSFQTKDLRCFVME 226
QY 192 YINGGELFYHLORCFLEPRARYAAEIASALGYLHSLNIVYRDLPENILDSQGHV 251
DB 227 YVNGGELFFHLRSERVSERTRFYGAIVSALDYLSGKIVYRDLEKLEMLDKGCHIK 286
QY 252 LTDFGLCKENIEHNTSTTSCGTPEYLAPEVLHKQPYDRYVDMWCLGAVLYEMLYGLPPF 311
DB 287 ITDFGLCKEGITDAATMKTTCGTPEYLAPEVLEDNDYGRAVDWMLGVVYMWNCGLRPF 346
QY 312 YSRNTAEYNYNLKPLQKPNITNSARHLEGLLQKDKTKRL-GAKDDPWEIKSHVFFS 370
DB 347 YNQDHEKLFELLIMEDIKFPRTLSSDAKSLSLGLLINDPNKRLGGGPDPAKEIMRHSFFS 406

RESULT 6

AKT3_MOUSE
ID AKT3_MOUSE STANDARD; PRT; 479 AA.
AC G9WUA6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RAC-gamma serine/threonine protein kinase (EC 2.7.1.-) (RAC-PK-gamma)
GN (Protein kinase Akt-3) (Protein kinase B, gamma) (PKB gamma).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RX MEDLINE=99194749; PubMed=10092583;
RA Brodbeck D., Cron P., Hemmings B.A.;
RT "A human protein kinase B gamma with regulatory phosphorylation sites
in the activation loop and in the C-terminal hydrophobic domain.";
RL J. Biol. Chem. 274:9133-9136(1999).
RN [2]
RX SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RP TISSUE=Brain;
RP PubMed=11387345;
RA Brodbeck D., Hill M.M., Hemmings B.A.;
RT "Two splice variants of PKB gamma have different regulatory capacity
depending on the presence or absence of the regulatory phosphorylation
site Ser 472 in the C-terminal hydrophobic domain.";
RL J. Biol. Chem. 276:29550-29558(2001).
CC -1- FUNCTION: IGF-1 LEAD TO THE ACTIVATION OF AKT3, WHICH MAY PLAY A
ROLE IN REGULATING CELL SURVIVAL. CAPABLE OF PHOSPHORYLATING
SEVERAL KNOWN PROTEINS. TRUNCATED ISOFORM 2/PKB GAMMA 1 WITHOUT
THE SECOND SERINE PHOSPHORYLATION SITE COULD STILL BE STIMULATED
BUT IN A LESSER EXTENT (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC AND MEMBRANE-ASSOCIATED AFTER
CELL STIMULATION LEADING TO ITS TRANSLOCATION. (SHOWN HERE) AND
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1/PKB GAMMA (SHOWN HERE) AND
2/PKB GAMMA 1; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: ISOFORM 1 IS EXPRESSED IN PROSTATE, TESTIS,
UTERUS AND MAMMARY GLAND AND ISOFORM 2 IS EXPRESSED IN PROSTATE,
TESTIS AND MAMMARY GLAND.
CC -1- DOMAIN: BINDING OF THE PH DOMAIN TO THE PHOSPHATIDYLINOSITOL 3-
KINASE ALPHA (PI(3)K) RESULTS IN ITS TARGETING TO THE PLASMA
MEMBRANE.
CC -1- PTM: PHOSPHORYLATED ON THREONINE AND SERINE RESIDUES.
CC -1- PHOSPHORYLATION ON BOTH SITES IS REQUIRED FOR FULL ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -1- RAC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -----
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CC -----
CC ENBL; AF124142; AAD29090.1; --
DR HSP; P05132; ICTP.
DR MGD; MGI:1345147; Akt3.
DR InterPro; IPR000719; Euk_pkinase.
DR

```

DR InterPro: IPR001849; PH.
DR InterPro: IPR000961; Pkinase C.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00169; PH; 1.
DR Pfam: PF00433; pkinase C; 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00233; PH; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
DR PROSITE: PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE: PS00003; PH_DOMAIN; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Alternative splicing.
FT DOMAIN 5 107
FT DOMAIN 148 405
FT NP BIND 154 162
FT BINDING 177 177
FT ACT SITE 271 271
FT MOD RES 305 305
FT MOD RES 472 472
FT VAR5PLIC 452 479
FT SEQUENCE 479 AA; 55714 MW; F08ACDF75743B8F CRC64;

Query Match 39.1%; Score 916; DB 1; Length 479;
Best Local Similarity 45.1%; Pred. No. 7e-57;
Matches 193; Conservative 67; Mismatches 140; Indels 28; Gaps 7;

Qy 33 SPFLSGLAFWKQRMGLNDFIQK-----IANNYSACKHPE-----VQSILKISQPO 78
Db 53 NFSVAKQLMKTKRPKPTFIIRCLQWTTVIERTFHTVDTPEEREWEATEIQAVADRLQ 112

Qy 79 EPELNNANPPSPSPSOQINLG---PSSNPHAK---PSDFHLKLVKGSGFGKVLARH 131
Db 113 EERNMCSPT-----SQIDNIGBEEMDASTTHHKRTMNDPDKLKGKTFGKVLVRE 167

Qy 132 KAEVEFYAVVLQKAIKKKEKHIMSERVLLKNVKKPPLVGLHFSFQTADKLYFVLD 191
Db 168 KASGKYAMKILKEVIIAKDEVAHTUTESRV-LKNTRHFPFLTSKYSFQTKDRLCFVME 226

Qy 192 YINGGELFYHLQRCLEPRARYAEIASALGYLSHIVRDLPENILDSQGHV 251
Db 227 YVNGGELFFHLRSERVSFSDTRFYGAIEVSALDYLSHGKIVYVRDLKLENMLDKGHK 286

Qy 252 LTDPLCKENIHNSTSTFCGTPPEYLAPVLLHKQPYDRTVDMWCLGAVLYEMLGLPPF 311
Db 287 ITDFGLCKEGITDAWTKTFCGTPPEYLAPVLEVDYGRAVDWGLGVNVEYEMCGELPP 346

Qy 312 YSRNTAEYDNIKNPLQKFNITNSARHLLEGLLQKDRTKRL-GAKDDFMEIKSHVFFS 370
Db 347 YNODHEKLFELLIMEDIKFPRTLSSDAKSLLSGLLIKDPNKLGGGPDDAKEIMRHSHFFS 406

Qy 371 LINWDDLINKITPPFPNVPNSGNDLRHDPPEPTEEPVPSIGKSPDSVLVTASVKEAE 430
Db 407 GVNWQDYVDKLVKPPFPQVTSSETDTRYFDDEEFTAQTTITTPPEKYDDMGDMGNRRP 466

Qy 431 AFLGFSVA 438
Db 467 HFQQFSYS 474

RESULT 7
AKT3 RAT
ID AKT3 RAT STANDARD; PRT; 454 AA.
AC Q63484;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE RAC-gamma serine/threonine protein kinase (EC 2.7.1.1-) (RAC-PK-gamma)
DE (protein kinase Akt-3) (protein kinase B, gamma) (PKB gamma).
GN AKT3
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96063640; PubMed=7488143;
RA Konishi H., Kuroda S., Tanaka M., Matsuzaki H., Ono Y., Kameyama K.,
RA Haga T., Kikkawa U.;
RT "Molecular cloning and characterization of a new member of the RAC
RT protein kinase family: association of the pleckstrin homology domain
RT of three types of RAC protein kinase with protein kinase C subtypes
RT and beta gamma subunits of G proteins.";
RL Biochem. Biophys. Res. Commun. 216:526-534 (1995).
CC -!- FUNCTION: IGF-1 LEAD TO THE ACTIVATION OF AKT3, WHICH MAY PLAY A
CC -!- ROLE IN REGULATING CELL SURVIVAL. CAPABLE OF PHOSPHORYLATING
CC SEVERAL KNOWN PROTEINS (BY SIMILARITY).
CC -!- DOMAIN: BINDING OF THE PH DOMAIN TO THE PHOSPHATIDYLINOSITOL 3-
CC KINASE ALPHA (PI(3)K) RESULTS IN ITS TARGETING TO THE PLASMA
CC MEMBRANE.
CC -!- PTM: PHOSPHORYLATED ON THREONINE AND SERINE RESIDUES.
CC PHOSPHORYLATION ON BOTH SITES IS REQUIRED FOR FULL ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. RAC
CC SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL: D49836; BAA08637.1; --
CC HSSP: P05132; LFMO.
CC InterPro: IPR000719; Euk_pkinase.
CC InterPro: IPR001849; PH.
CC InterPro: IPR000961; Pkinase C.
CC InterPro: IPR002290; Ser_thr_pkinase.
CC Pfam: PF00069; pkinase; 1.
CC Pfam: PF00169; PH; 1.
CC Pfam: PF00433; pkinase C; 1.
CC ProDom: PD000001; Euk_pkinase; 1.
CC SMART: SM00233; PH; 1.
CC SMART: SM00133; S_TK_X; 1.
CC SMART: SM00220; S_TKC; 1.
CC PROSITE: PS00107; PROTEIN KINASE ATP; 1.
CC PROSITE: PS00108; PROTEIN KINASE_ST; 1.
CC PROSITE: PS00011; PH_DOMAIN; 1.
CC PROSITE: PS00003; PH_DOMAIN; 1.
CC Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 5 107
FT DOMAIN 148 405
FT NP BIND 154 162
FT BINDING 177 177
FT ACT SITE 271 271
FT MOD_RES 305 305
FT SEQUENCE 454 AA; 52849 MW; 6B072CF9DFEE876 CRC64;

Query Match 38.9%; Score 910; DB 1; Length 454;
Best Local Similarity 47.0%; Pred. No. 1.7e-56;
Matches 187; Conservative 63; Mismatches 120; Indels 28; Gaps 7;

Qy 33 SPFLSGLAFWKQRMGLNDFIQK-----IANNYSACKHPE-----VQSILKISQPO 78
Db 53 NFSVAKQLMKTKRPKPTFIIRCLQWTTVIERTFHTVDTPEEREWEATEIQAVADRLQ 112

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Qy 79 EPELMANPSPSPSQINLG-----PSSNPHAK---PSDFHFLKVIKSGFGKVLARH 131
 Db 113 EERNMCSPT-----SOLDNIGEEEMDASTTHHRKTMNDPDLKLGKGTGKVLVRE 167
 Qy 132 KAEEVFVAVKQKAILKKKEEKHIMSERVLLKNVKKHPLVGLHFSFOTADKLYFVLD 191
 Db 168 KASQKYAMKILKEVIAKDEVATITESTV-LKTRHPFLTSKTSFQTKDRLCFWE 226
 Qy 192 YINGELFYHLQRCFLPRARYAAIASALGYLHSLNIVYRDLKPNILLDSOGHIV 251
 Db 227 YVNGELFFHLRSRVSFSDTRFYGAIVSALDYHSGKIVYRDLKLENLMDKDGHIK 286
 Qy 252 LTDFGLCKENIEHNSSTSTFCGTPYLAPEVLHQPDRYVDMWCLGAVLYEMLYGLPPF 311
 Db 287 ITDFGLCKEGITDAATWKTFCTGTPYLAPEVLENDYGRAVDMWGLGVMMYEMMCGRLPF 346
 Qy 312 YSRNTAEYONILNKPLQKNPNTNSARHLLGLELQKDRKRL-GAKDDFMEIKSHVFFS 370
 Db 347 YNQDHEKLPFELLMEDIKFRTLSDDAKSLLSGLLIDKPNKRLGGGDDPKKIMRHSFFS 406
 Qy 371 LINWDDLINKKITPPFNPVNSGPNDLRHFDPEFTEEPV 408
 Db 407 GVNQDVYDKLVPPFKPQVTSSETDTRYDFDEEFTAQTI 444

RESULT 8
 KRAC RAT
 ID KRAC RAT STANDARD; PRT; 480 AA.
 AC P47196;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 13-JUN-2002 (Rel. 41, Last annotation update)
 DE RAC-alpha serine/threonine kinase (EC 2.7.1.-) (RAC-PK-alpha)
 DE (protein kinase B) (PKB).
 GN AKT1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=95091823; PubMed=7999118;
 RA Konishi H., Shinomura T., Kuroda S.I., Ono Y., Kikkawa U.;
 RT "Molecular cloning of rat RAC protein kinase alpha and beta and their
 RT association with protein kinase C zeta.";
 RL Biochem. Biophys. Res. Commun. 205:817-825(1994).
 CC -I- FUNCTION: General protein kinase capable of phosphorylating
 CC several known proteins.
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic and nuclear after activation by
 CC integrin-linked protein kinase 1 (ILK1) (By similarity).
 CC -I- TISSUE SPECIFICITY: Widely expressed. Low levels found in liver
 CC with slightly higher levels present in thymus and testis.
 CC -I- DOMAIN: Binding of the ph domain to the phosphatidylinositol 3-
 CC kinase alpha (PI(3)K) results in its targeting to the plasma
 CC membrane.
 CC -I- PTM: Phosphorylation on Thr-308 and Ser-473 is required for full
 CC activity.
 CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC RAC SUBFAMILY.
 CC -I- SIMILARITY: CONTAINS 1 PH DOMAIN.
 CC -----
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 CC or send an email to license@sb-sib.ch).
 CC -----
 CC EMBL; D30040; BAA06279.1; --
 CC HSP; P05132; ICTP.
 DR InterPro; IPR000719; Euk_pkinase.
 DR

DR InterPro; IPR001849; PH.
 DR InterPro; IPR000961; Kinase C.
 DR InterPro; IPR002290; Ser thr_pkinase.
 DR Pfam; PF00069; kinase; 1.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00433; kinase C; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TK; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00003; PH_DOMAIN; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 KW DOMAIN 5 108 PH.
 FT DOMAIN' 150 408 PROTEIN KINASE.
 FT NE_BIND 156 164 ATP (BY SIMILARITY).
 FT BINDING 179 179 ATP (BY SIMILARITY).
 FT ACT_SITE 274 274 BY SIMILARITY.
 FT MOD_RES 308 308 PHOSPHORYLATION (BY PDPK1) (BY
 FT SIMILARITY).
 FT MOD_RES 473 473 PHOSPHORYLATION (BY ILK1) (BY
 FT SIMILARITY).
 SQ SEQUENCE 480 AA; 55735 MW; 5DCAAE7134366D04 CRC64;
 Query Match 37.5%; Score 878; DB 1; Length 480;
 Best Local Similarity 41.9%; Pred.No.3.2e-54;
 Matches 191; Conservative 81; Mismatches 146; Indels 38; Gaps 10;
 Qy 18 RPR-----HKRAEAQKRSES-----FLSLGAFMKQRMGLNDFIQK----- 55
 Db 23 RRYVFLKNDGTFTGYKERPDQVQRESPLNNSVAQCQLMKTERPRPNTFIIRCLQWTT 82
 Qy 56 IANNSVACKPE-----VQSILKISQDPELMNANSPPP--SPSQINLGPSNP 105
 Db 83 VIBRTFHVETPEEREETTAIQTVADGLKQEEETMDFRSGSPSDNSGAEEMEAVALAKPK 142
 Qy 106 H-AKPSDFHFLKVIKSGFGKVLARHKAEEVYAVKVLQKAILKKKEKHIMSERVNL 164
 Db 143 HRVTMNEFEYKLGKGTGKVLVKEKATGRYAMKILKEVIAKDEVATILTE-NRV 201
 Qy 165 LKNVHFPFLVGLHFSFQTDKLYFVLDYINGGELFYHLQRCFLPRARYAAEIASAL 224
 Db 202 LQNSRHPFLTALKVYSFQTHDRLCFVMEYANGGELFFHLRSRVSFSDTRFYGAIEVSAL 261
 Qy 225 GYLHS-LNIVYRDLKPNILLDSQGHIVLTDPLCKENIEHNSSTSTFCGTPYLAPEVL 283
 Db 262 DYLSHSEKNVYRDLKLENLMDKDGHIKITDFGLCKEGIKDGATMKTFCGTPYLAPEVL 321
 Qy 284 HKQDPYDRTVDMWCLGAVLYEMLYGLPPFSRNTAEYONILNKPLQKNPNTNSARHLE 343
 Db 322 EDNDYGRADVMMGLGVMMYEMMCGRLPFYNQDHEKLPFELLMEIRPPTGLSGPEAKSLLS 381
 Qy 344 GLLQKDRKRL-GAKDDFMEIKSHVFFSLINWDDLINKKITPPFNPVNSGPNDLRHFDPE 402
 Db 382 GLLKKDPTQLRGSGSEDAKEIMQHRFFANIVMDVVEKKLSPFPKQVTSSETDTRYDEE 441
 Qy 403 FTEEPVNSIGKSPDSVLVTASVKAEAEAPLGSYA 438
 Db 442 FTAQMITITPPDDDSMECVDS--ERRPHFPQFSYS 475

RESULT 9
 RAKT_MLVAT
 ID RAKT_MLVAT STANDARD; PRT; 501 AA.
 AC P31748;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE AKT kinase transforming protein (EC 2.7.1.-).
 GN V-AKT.

OS AKT8 murine leukemia virus.
 CC Viruses; Retroviral viruses; Retroviridae; Gammatetovirus.
 OX NCBI_TaxID=11790;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92022574; PubMed=1833819;
 RA Bellacosa A., Testa J.R., Staal S.P., Teichlis P.N.;
 RT "A retroviral oncogene, akt, encoding a serine-threonine kinase
 containing an SH2-like region.";
 RL Science 254:274-277(1991).
 CC -1- PFM: AUTOPHOSPHORYLATED ON THR AND SER RESIDUES.
 CC -1- MISCELLANEOUS: THIS PROTEIN IS EXPRESSED AS A FUSED GAG-AKT
 CC POLYPROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC RAC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
 CC
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 CC
 CC EMBL; M80675; AAA42545.1; --
 CC PIR; B40831; KIMVT8.
 CC HSP; P05132; ICTP.
 CC InterPro; IPR000719; Euk_pkinase.
 CC InterPro; IPR001849; PH.
 CC InterPro; IPR000961; Pkinase_C.
 CC InterPro; IPR002290; Ser_thr_pkinase.
 CC Pfam; PF00069; Pkinase_1.
 CC Pfam; PF00169; PH; 1.
 CC Pfam; PF00433; Pkinase_C; 1.
 CC ProDom; PD000001; Euk_pkinase; 1.
 CC SMART; SM00233; PH; 1.
 CC SMART; SM00133; S TK X; 1.
 CC SMART; SM00220; S TK; 1.
 CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 CC PROSITE; PS00108; PROTEIN KINASE ST; 1.
 CC PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
 CC PROSITE; PS00003; PH DOMAIN; 1.
 CC Oncogene; Transferase; Serine/threonine-protein kinase;
 CC Phosphorylation; ATP-binding;
 CC FT DOMAIN 26 129 PH.
 CC FT DOMAIN 171 429 PROTEIN KINASE.
 CC FT NP_BIND 177 185 ATP (BY SIMILARITY).
 CC FT BINDING 200 200 ATP (BY SIMILARITY).
 CC FT ACT_SITE 295 295 BY SIMILARITY.
 CC FT MOD_RES 347 347 PHOSPHORYLATION (BY SIMILARITY).
 CC SQ SEQUENCE 501 AA; 57870 MW; 5845658CD42F73 CRC64;
 Query Match 37.5%; Score 878; DB 1; Length 501;
 Best Local Similarity 41.9%; Pred. No. 3.4e-54;
 Matches 194; Conservative 77; Mismatches 140; Indels 52; Gaps 11;
 QY 18 RPR-----HKRAEAQKRS-----FLLSGLAFWKQRMGLNDFIQK----- 55
 DB 44 RPRYFLKNDGTFIGYKERPDQVQDRESPLNFVSAQCQLMKTERPRENTFIIRCLQWTT 103
 QY 56 IANNYSACKHPE-----VQSITKISQOPEELMANPSPSPS-----QQINLGPSS 103
 DB 104 VIERTFHVTEPEEREWEATAITQVADGLKQKEETMDFRSGPSDNGAEMEVSU----- 159
 QY 104 NPAKP-----SDFHLKLVIGKSGFGKVLARHAKAEVYAVKVLQKAILKKKEEKHI 157
 DB 160 ---AKPRHRTVMNEFEYLLKLGKTFGKVLVKEKATGRYVAMKILKEVIAKDEVAHT 216
 QY 158 MSERNVLKXVKKHFLVGLHFSFOTADKLYFLVDLYINGGELFYHLQRCFLEPRARFYA 217
 DB 217 LTE-NRVLQNSRHPFLTALKYSFQTHDLRCFMEYANGGELFFHLFSRVSFEDRARFYG 275

RESULT 10

KRAC_MOUSE
 ID KRAC_MOUSE STANDARD; PRT; 480 AA.
 AC P31750; Q62274;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE RAC-alpha serine/threonine kinase [EC 2.7.1.1-] (RAC-PK-alpha) (AKT1
 DE kinase) (Protein kinase B) (PKB) (C-AKT) (Thymoma viral proto-
 DE oncogene).
 DE GN AKT1 OR AKT OR RAC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bousquets X., Powell C.;
 RL Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RC STRAIN=AKR/J; TISSUE=Thymus;
 RX MEDLINE=93173519; PubMed=8437858;
 RA Bellacosa A., Franke T.F., Gonzalez-Portal M.E., Datta K., Taguchi T.,
 RA Gardner J., Cheng J.Q., Testa J.R., Teichlis P.N.;
 RT "Structure, expression and chromosomal mapping of c-akt: relationship
 RT to v-akt and its implications.";
 RC Oncogene 8:745-754(1993).
 CC -1- FUNCTION: General protein kinase capable of phosphorylating
 CC several known proteins.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear after activation by
 CC integrin-linked protein kinase 1 (ILK1) (By similarity).
 CC -1- TISSUE SPECIFICITY: Widely expressed. Low levels found in liver
 CC with slightly higher levels present in thymus and testis.
 CC -1- DOMAIN: Binding of the ph domain to the phosphatidylinositol 3-
 CC kinase alpha (PI(3)K) results in its targeting to the plasma
 CC membrane.
 CC -1- PTM: Phosphorylation on Thr-308 and Ser-473 is required for full
 CC activity.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC RAC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M94335; AAA18254.1; --
 CC EMBL; X55687; CAA46620.1; --
 CC HSP; P05132; ICTP.
 CC MGI; MGI:87986; Akt1.
 CC InterPro; IPR000719; Euk_pkinase.

RESULT 11

Db 292 ITDFGLSKK-IETDTGFTFCGTEPYLAPEVLNGHGHGCAVDWMSLGLTLLYEMLTGLPPF 350
 QY 312 YSRNTAWYDNLNKLQKPNITNSARHLLEGLOKDRKRLGAKDDFWEIKSHVPSFL 371
 Db 351 YQNVSTMYOKILNGELUKPTYISPEAKSLLEGULLTREVDRRLGTGG-GEVQHPWFKN 409
 QY 372 INWDLINKITPPFNVSQPNDRHFDPEFTTEPVPNSIGKSPDPSVLVTASVKEAA-- 429
 Db 410 IDWEKLORKEVHFHFKPKVSGTDSIQDPVFTQE-----RPMDSLVETSALGDAMGK 462
 QY 430 -EAPLGSYAPPTDSFL 445
 Db 463 DTSFEGTYV--ADSIL 477

RESULT 12

AKT2_HUMAN STANDARD; PRT; 481 AA.
 AC P31751;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE RAC-beta serine/threonine protein kinase (EC 2.7.1.1-) (RAC-PK-beta)
 DE (Protein kinase Akt-2) (Protein kinase B, beta) (PKB beta).
 GN AKT2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Epithelium;
 RX MEDLINE=92198987; PubMed=1801921;
 RA Jones P.F., Jakubowicz T., Hemmings B.A.;
 RT "Molecular cloning of a second form of rac protein kinase."
 RL Cell Regul. 2:1001-1009 (1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9302845; PubMed=1409633;
 RA Cheng J.Q., Godwin A.K., Bellacosa A., Taguchi T., Franke T.F.,
 Hamilton T.C., Tsichlis P.N., Testa J.R.;
 RT "AKT2, a putative oncogene encoding a member of a subfamily of
 RT protein-serine/threonine kinases, is amplified in human ovarian
 RT carcinomas."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:9267-9271 (1992).
 CC -1- FUNCTION: GENERAL PROTEIN KINASE. CAPABLE OF PHOSPHORYLATING
 CC SEVERAL KNOWN PROTEINS.
 CC -1- TISSUE SPECIFICITY: IN ALL HUMAN CELL TYPES SO FAR ANALYZED.
 CC -1- DISEASE: ALTERATIONS OF AKT2 MAY CONTRIBUTE TO THE PATHOGENESIS OF
 CC OVARIAN CARCINOMAS.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC RAC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M7198; AAA36585.1; -;
 DR EMBL; M95936; AAA58364.1; -;
 DR PIR; A46288; A46288.
 DR HSP; P05132; IAPM.
 DR Genew; HGNC:392; AKT2.
 DR MIM; 164731; -;
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.

DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00433; pkinase_C; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00133; S_TK; 1.
 DR SMART; SM00220; S_TK; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50003; PH_DOMAIN; 1.
 KW transferase; Serine/threonine-protein kinase; ATP-binding.
 FT DOMAIN 5 108 PH.
 FT DOMAIN 152 409 PROTEIN KINASE.
 FT NP_BIND 158 166 ATP (BY SIMILARITY).
 FT BINDING 181 181 ATP (BY SIMILARITY).
 FT ACT_SITE 275 275 BY SIMILARITY.
 FT ACT_SITE 478 481
 FT CONFLICT 478 481
 FT SIRE -> FREEKDLMSLVSVLILFSDFSLSKSHSFSSNF
 FT ILLSFSLKK (IN REF. 1).
 SQ SEQUENCE 481 AA; 55768 MW; B18C87A7246BF24 CRC64;
 Query Match 36.9%; Score 863.5; DB 1; Length 481;
 Best Local Similarity 42.6%; Pred. No. 3.3e-53;
 Matches 182; Conservative 70; Mismatches 138; Indels 37; Gaps 7;
 QY 18 RPR-----HKRAEAKRS-----ESFLSGLAFMKQRMGLNDFIOK----- 55
 Db 23 RPRYFLKSDSGFIGYKERPEAPDQTLPLNNFSAECQLMKTERPRPNTFVIRCLQWTT 82
 QY 56 IANNSYACKHPE-----VQSILKISQPEPELMNANSPSPSPSQNLGPPSSN 104
 Db 83 VIERTFHVSDPDREEREMRAIOMVANSKQAPGEDPMYKCGSPSDSSTTEMEVAVSK 142
 QY 105 PHAK--PSPDFHLKVLGKSGFGLARHKAEEVFYAVKVLQKAILKKKEKHIMSE 162
 Db 143 ARAKVTMNDFDYLLGLGKGTGKVLVREKATGRYAMKILRKEVIIAKDEVAHTVTSR 202
 QY 163 VLLKNVHPFLVGLHFSFQTADKLYEVLVDYINGELFYHLQRCFLEPRARYAABIAS 222
 Db 203 V-LQNRHPFLTALKYAFQTHDLRCFVMEYANGELFFHLRSRVTEERARYGAEIVS 261
 QY 223 ALGYLSLNIIVRDLPENILDSQGHIVLTDGLCKENIEHNSTSTFCGTPEYLAPEV 282
 Db 262 ALEYLSHRDVVYRDIKLENLMLDKGHIKITDGLCKEGISDGTATWKTFCGTPEYLAPEV 321
 QY 283 LHKQPVDRVTDMVCLGAVLYEMLYGLPPFVSRNTAEWYDNLNKLQKPNITNSARHLL 342
 Db 322 LEDNDYGRAVDMWGLGVVMTEMMCGRLPFYVQDHERLDFELILMEEIRFPRTLSPKAKSL 381
 QY 343 EGLLQDRTKRL-GAKDDFMEIKSHVFFSLINWDDLINKKITPPFNPNVSGPNDLRHFD 401
 Db 382 AGLKKDKPKQRLGGGSDAKEVMEHFFLSINWQDVVQKLLPPFKPQVTSEVDTRYFDD 441
 QY 402 EFTTEPV 408
 Db 442 EFTAQSI 448

RESULT 13

KRAC_BOVIN STANDARD; PRT; 480 AA.
 ID KRAC_BOVIN
 AC Q01314;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE RAC-alpha serine/threonine kinase (EC 2.7.1.1-) (RAC-PK-alpha)
 DE (Protein kinase B) (PKB).
 GN AKT1 OR PKB.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=92037600; PubMed=1718748;
 RA Coffey P.J., Woodgett J.R.;
 RT "Molecular cloning and characterization of a novel putative protein-serine kinase related to the cAMP-dependent and protein kinase C families";
 RL Eur. J. Biochem. 201:475-481(1991).
 RN [2]
 RP REVISIONS.
 RX MEDLINE=92249329; PubMed=1533586;
 RA Coffey P.J., Woodgett J.R.;
 RL Eur. J. Biochem. 205:1217-1218(1992).
 CC -1- FUNCTION: General protein kinase capable of phosphorylating several known proteins.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear after activation by integrin-linked protein kinase 1 (ILK1).
 CC -1- DOMAIN: Binding of the ph domain to the phosphatidylinositol 3-kinase alpha (PI(3)K) results in its targeting to the plasma membrane.
 CC -1- PTM: Phosphorylation on Thr-308 and Ser-473 is required for full activity.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC RAC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
 CC
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 CC
 DR EMBL; X61036; CAA43371.1; -
 DR HSP; P05132; ICTP
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00433; pkinase_C; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50003; PH_DOMAIN; 1.
 DR Transferase; Serine/threonine-protein kinase; ATP-binding; phosphorylation.
 KW DOMAIN 5 108 PH.
 FT DOMAIN 150 408 PROTEIN KINASE.
 FT NP_BIND 156 164 ATP (BY SIMILARITY).
 FT BINDING 179 179 ATP (BY SIMILARITY).
 FT ACT_SITE 274 274 BY SIMILARITY.
 FT MOD_RES 308 308 PHOSPHORYLATION (BY PDPK1).
 FT MOD_RES 473 473 PHOSPHORYLATION (BY ILK1).
 SQ SEQUENCE 480 AA; 55617 MW; 0BACA4123EDSA848 CRC64;
 Query Match 36.8%; Score 862; DB 1; Length 480;
 Best Local Similarity 41.08; Pred. No. 4.2e-53;
 Matches 190; Conservative 80; Mismatches 111; Indels 52; Gaps 11;
 QY 18 RPR-----HKRAEAKRSES-----FLSLGLAFMKQRMGLNDFIQK----- 55
 DB 23 RPRVFLKNDGTFGYKERPDQLRQESPLNFSVAQQLMKTERPRPNTFIIRCLQWTT 82
 QY 56 IANNSYACKUPE-----VQSLKLSQPEPELMANFSPSPS-----QQINLGPS 103
 DB 83 VIERTFHVTEPEREWTIAITQVADGLKRQEEETMDFRSGSPGENSEGAEEMVSL----- 138

QY 104 NPAKP-----SDFHLKVIKSGFKVLLARHKAEEVYAVVKVLOKAILKKKEKHI 157
 DB 139 ---AKPKHRVTMNEFEYKLLGKTEGKVLVKEKATAAYYAMKILKEVIVAKDEVAHT 195
 QY 158 MSERNVLLKNVHKPFLVGLHFSQTDADKLVFLVDYINGGELFYHLOQRERCFLEPRARFYA 217
 DB 196 LTV-NRVLQNSRHPSLTALKYSPQTHDRJLCFVMEYANGELFFHLGRVFSRVEDRAFPYG 254
 QY 218 AEIASALGYLHS-LNIVYRDLKPKENILDSQGHVLTDFGLCKENIEHNSTTSTFCGTPE 276
 DB 255 AEIVSALDYLHSEKEVYRDLKLENLMDKDGHIKITDFGLCKEGIKDGATMTKTCGTPE 314
 QY 277 YLAPEVLHKOPYDRVTVMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKLQKPNITN 336
 DB 315 YLAPEVLENDYDGRAVDWMLGVMYVMMCGRLPFYFNQDHEKLFELILMEIRFPRTLS 374
 QY 337 SARHLEGLLOKDRKRL-CAKDDFMELKSHVFSLLINWDDLINKKITPFPNPNVSPND 395
 DB 375 EAKSLUSGLLKDKPKQRLGGSGSEDAKIMQHRFFASIVQDVYKLSPPPKPOVTSETD 434
 QY 396 LRHFDPEFTEEPVNSIGKSPDSVLVTASVKEAAEAFLGFSYA 438
 DB 435 TRYFDEFTAQMITITPPDDDSMEGVDS--ERRPHFPQFSYS 475
 RESULT 14
 ID AKT2 MOUSE STANDARD; PRT; 481 AA.
 AC Q60823; 2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE RAC-beta serine/threonine protein kinase (EC 2.7.1.-) (RAC-PK-beta)
 DE (Protein kinase Akt-2) (Protein kinase B, beta) (PKB beta).
 GN AKT2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
 RX MEDLINE=96032568; PubMed=7566964;
 RA Altomare D.A., Guo K., Cheng J.Q., Sonoda G., Walsh K., Testa J.R.;
 RT "Cloning, chromosomal localization and expression analysis of the mouse Akt2 oncogene".
 RL Oncogene 11:1055-1060(1995).
 CC -1- FUNCTION: GENERAL PROTEIN KINASE CAPABLE OF PHOSPHORYLATING SEVERAL KNOWN PROTEINS.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC RAC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
 CC
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 CC
 DR EMBL; U22445; AAA83557.1; -
 DR HSP; P05132; ICTP.
 DR MGD; MGI:104874; Akt2.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00433; pkinase_C; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.

DR SMART; SM00233; PH; 1.
 DR SMART; SM00133; S TK X; 1.
 DR SMART; SM00220; S TK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00003; PH_DOMAIN; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding.
 FT DOMAIN 5 108 PH.
 FT DOMAIN 152 409 PROTEIN_KINASE.
 FT NP_BIND 158 166 ATP (BY SIMILARITY).
 FT BINDING 181 181 ATP (BY SIMILARITY).
 FT ACT_SITE 275 275 BY SIMILARITY.
 SQ SEQUENCE 481 AA; 55741 MW; 4AB4A9C4FB9CFA7D CRC64;
 Query Match 36.8%; Score 861.5; DB 1; Length 481;
 Best Local Similarity 42.4%; Pred. No. 4.5e-53;
 Matches 181; Conservative 71; Mismatches 138; Indels 37; Gaps 7;
 QY 18 RPR-----HKRAEAQKRS-----ESFLLSGLAFMKQRRMGLNDFIOK----- 55
 DB 23 RPRFLKSDGSFGYKRPDPQTLPLNPNFSAECQLMKTFRPNTFVIRCLQWTT 82
 QY 56 IANNSYACKHPE-----VQSILKISQPEPELMNANPPPPSPSQQINLGSSN 104
 DB 83 VIERTFHVDSPEREENWRAIQMVANSIKQKRGCEADMDYKCGSPSDSTSEMMEVAVNK 142
 QY 105 PHAK--PSDFHFLKVGKSGKVLARHKAEEVYAVKVLQKAIILKKKEKHIMSEIN 162
 DB 143 ARAKVTWDFDYLKLLGKTGKVLVREKATGRYAMKILRKEVIIAKDEVAHTVTESR 202
 QY 163 VLLKNVHPFVLGLHFSQFADKLYFLVDYINGELFVHLQRECFLEPRARFYAAIAS 222
 DB 203 V-LQNRHPFALTAKYAFQTHDRLCFVWEVANGELFFHLRSERVFTEDRARFYGAIIVS 261
 QY 223 ALGYLHSLNIVYRDKPENILLDSQGHIVLTDLFGCKENIEHNSSTTFCGTPEYLAPEV 282
 DB 262 ALEYLHSDRVVYRDKLENMLDKDGHKITDFGLCKEGISDGMATKTCGTPEYLAPEV 321
 QY 283 LHKOPYDRTVDWCLGAVLHMLYGLPFFYSRNTAEYMDNLNLPQLKKNITNSARHLL 342
 DB 322 LEDNDYGRADVWGLGVVYEMMCGRLPFYQNDGHERLFEILMEIEIPRTLGPAAKSL 381
 QY 343 EGLQKDKTKRL-CAKDDFWEIKSHVFSLINWDLINKKITPPFNPNVSGPNDLRHFD 401
 DB 382 AGLLKDPKQLGSGPSDAKEVMEHRPFLSINWQDVVQKLLPFKQVTSVDVTRTFDD 441
 QY 402 EFTPEEPV 408
 DB 442 EFTAQSI 448

RESULT 15
 KRAC HUMAN STANDARD; PRT; 480 AA.
 AC P31749;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE RAC-alpha serine/threonine kinase (EC 2.7.1.-) (RAC-PK-alpha)
 DE (Protein kinase B) (PKB) (C-AKT)
 GN AKT1 OR RAC OR PKB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91239529; PubMed=1851997;
 RA Jones P.F., Jakubowicz T., Pirossi F.J., Maurer F., Hemmings B.A.;
 RT "Molecular cloning and identification of a serine/threonine protein
 RT kinase of the second-messenger subfamily.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:4171-4175(1991).

RN [2]
 RP SEQUENCE FROM N.A.
 RA Matsubara A., Wasson J., Donelan S., Wellington C., Permutt A.;
 RT "Human AKT1 gene: characterization of genomic structure and
 RT identification of single nucleotide polymorphisms (SNPs).";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 63-480 FROM N.A.
 RC TISSUE=Foreskin;
 RX MEDLINE=92037600; PubMed=1718748;
 RA Coffey P.J., Woodgett J.R.;
 RT "Molecular cloning and characterisation of a novel putative protein-
 RT serine kinase related to the CAMP-dependent and protein kinase C
 RT families.";
 RL Eur. J. Biochem. 201:475-481(1991).
 RN [4]
 RP REVISIONS.
 RX MEDLINE=92249329; PubMed=1533586;
 RA Coffey P.J., Woodgett J.R.;
 RL Eur. J. Biochem. 205:1217-1218(1992).
 RN [5]
 RP CHARACTERIZATION.
 RX MEDLINE=98409636; PubMed=9736715;
 RA Delcommenne M., Tan C., Gray V., Rue L., Woodgett J.R., Dedhar S.;
 RT "Phosphoinositide-3-OH kinase-dependent regulation of glycogen
 RT synthase kinase 3 and protein kinase B/AKT by the integrin-linked
 RT kinase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:11211-11216(1998).
 RN [6]
 RP MUTAGENESIS OF THR-308 AND SER-473, AND PHOSPHORYLATION OF THR-308 AND
 RP SER-473.
 RX MEDLINE=97133284; PubMed=8978681;
 RA Alessi D.R., Andjelkovic M., Caudwell F.B., Cron P., Morrice N.,
 RA Cohen P., Hemmings B.A.;
 RT "Mechanism of activation of protein kinase B by insulin and IGF-1.";
 RL EMBO J. 15:6541-6551(1996).
 CC -1- FUNCTION: General protein kinase capable of phosphorylating
 CC several known proteins.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear after activation by
 CC integrin-linked protein kinase 1 (ILK1).
 CC -1- TISSUE SPECIFICITY: In all human cell types so far analyzed.
 CC -1- DOMAIN: Binding of the ph domain to the phosphatidylinositol 3-
 CC kinase alpha (PI(3)K) results in its targeting to the plasma
 CC membrane.
 CC -1- PTM: Phosphorylation on Thr-308 and Ser-473 is required for full
 CC activity.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC RAC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL; MG3167; AAA36539.1; -.
 CC DR EMBL; AF283830; AAL55732.1; -.
 CC DR EMBL; AF283819; AAL55732.1; JOINED.
 CC DR EMBL; AF283820; AAL55732.1; JOINED.
 CC DR EMBL; AF283821; AAL55732.1; JOINED.
 CC DR EMBL; AF283822; AAL55732.1; JOINED.
 CC DR EMBL; AF283823; AAL55732.1; JOINED.
 CC DR EMBL; AF283824; AAL55732.1; JOINED.
 CC DR EMBL; AF283825; AAL55732.1; JOINED.
 CC DR EMBL; AF283826; AAL55732.1; JOINED.
 CC DR EMBL; AF283827; AAL55732.1; JOINED.
 CC DR EMBL; AF283828; AAL55732.1; JOINED.
 CC DR EMBL; AF283829; AAL55732.1; JOINED.
 CC DR EMBL; X61037; CAA43372.1; -.
 CC DR PIR; A39360; A39360.

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DR HSP; POS132; ICTP.
DR Genew; HGNC:391; AKT1.
DR MIN; 164730; -
DR InterPro; IPR001849; PH_pkinase.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00169; PH; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS50003; PH DOMAIN; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Nuclear protein.
FT DOMAIN 5 108
FT DOMAIN 150 408
FT NP_BIND 156 164
FT BINDING 179 179
FT ACT_SITE 274 274
FT MOD_RES 308 308
FT MOD_RES 473 473
FT MUTAGEN 308 308
FT MUTAGEN 473 473
FT MUTAGEN 473 473
FT CONFLICT 173 174
FT CONFLICT 202 202
FT CONFLICT 212 212
FT CONFLICT 246 246
FT CONFLICT 409 409
FT CONFLICT 476 476
FT CONFLICT 478 478
SQ SEQUENCE 480 AA; 55716 MW; 6EAF938AD436714 CRC64;

Query Match 36.8%; Score 861; DB 1; Length 480;
Best Local Similarity 42.3%; Pred. No. 4.9e-53;
Matches 189; Conservative 76; Mismatches 144; Indels 38; Gaps 10;

Qy 18 RPHKKAQAQKSEFLLSGLAEWKORRMCLNDFIQK-----IANNVACKHPE---- 67
Db 41 RPQVDQREAP--LNNFSVAQCQLMKTERPRNTFIIRCLQMTTIVERTFHVETPEERE 98
Qy 68 ----VQSILKISQPEPELMANPPPPSPS---QQINLGPSNPHAKP-----SDFH 113
Db 99 WTTATQTVADGLKKQEEEMDFRSGSPSDNSGAEMEVS-----AKPKHRTVMNEFE 151
Qy 114 FLKVIKSGFKVLLARHKAEEVYAVKVLQKKAIIKKKEKHIMSERNVLLKNVGHFFL 173
Db 152 YLKLKLGKGTGKVLVKEKATGRYYAMKILKEVIVAKDEVAHTLTE--NRVLQNSRHFFL 210
Qy 174 VGLHFSQTADKLYFLVDYNGGELFYHLORCERCFLEPRARFYAEIASALGYLHS--LNI 232
Db 211 TALKYSPQTHRLCFVMYANGGELFFHLGRVFSERDRARFYGAIEVSALDYLHSEKNV 270
Qy 233 VYRDLKPENILDSQGHIVLTDGCLCKENIEHNSTTFTCGTPEYLAPEVLHKQPYDRTV 292
Db 271 VYRDLKLENLMDKDGHIKITDFGLCKEGIKDGATMTTCCTPEYLAPEVLEDNDYGRAV 330
Qy 293 DWKCLGAVLYEMLYGLPPFYSRNTAEYDNIINLKPLQKNITNSARHLLGLELQKDRTK 352
Db 331 DWKGLGVVYEMMCGRLPPFYNQDHEKLFELILMEEIRPPTLGPGEAKSLLSGLLKKDPKQ 390
Qy 353 RL-GAKDDPFMEIKSHVFFSLINWDLINKKITPPFNPNVSGPNDLRHDFDEFTPEEPVNS 411
Db 391 RLGGSSEDAKEIMQHRPFAGIVQHVYKELSPFPKQVTSQVTDTRYFDEEFTAQMITIT 450
```

Qy 412 IGKSPDSVLVTASVKAAAEAFGLGFSYA 438
|||:|:|:|:
Db 451 PPQDDDSMECVDS--ERRPHFPQFSYS 475

Search completed: June 20, 2003, 19:25:16
Job time : 25 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2003, 19:22:28 ; Search time 42 Seconds
(without alignments)
1018.567 Million cell updates/sec

Title: US-10-067-977-2
Perfect score: 2340
Sequence: 1 MGENQALARLESLLRPR.....KEAAEAFGLFSYAPPTDSFL 445
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 73.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2118	90.5	431	2	serum and glucocor
2	1082	46.2	422	2	hypothetical prote
3	916	39.1	479	1	protein kinase (EC
4	912	39.0	462	1	protein kinase (EC
5	910	38.9	454	1	protein kinase (EC
6	894	38.2	611	1	protein kinase (EC
7	878	37.5	480	1	protein kinase (EC
8	878	37.5	480	1	protein kinase (EC
9	878	37.5	763	1	gag-akt polyprotei
10	864.5	36.9	479	2	protein kinase 2 (
11	863.5	36.9	481	1	protein kinase (EC
12	862	36.8	480	1	protein kinase (EC
13	861	36.8	480	1	protein kinase (EC
14	852.5	36.4	481	1	protein kinase (EC
15	831.5	35.5	677	2	protein kinase YKR
16	828	35.4	569	2	probable prolifera
17	827.5	35.4	680	2	protein kinase YPK
18	814	34.8	546	1	protein kinase (EC
19	812	34.7	481	2	p70 S6 kinase (EC
20	807	34.5	525	1	ribosomal protein
21	807	34.5	525	1	probable ribosomal
22	801.5	34.3	541	1	protein kinase (EC
23	799	34.1	634	1	protein kinase C (
24	798	34.1	525	1	ribosomal protein
25	796.5	34.0	1016	1	protein kinase C (
26	791.5	33.8	672	1	protein kinase C (
27	791.5	33.8	672	1	protein kinase C (
28	791.5	33.8	672	1	protein kinase C (
29	790.5	33.8	672	1	protein kinase C (

ALIGNMENTS

RESULT 1

A48094
serum and glucocorticoid-regulated kinase - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 19-Dec-1997
C;Accession: A48094
R;Webster, M.K.; Goya, L.; Ge, Y.; Maiyar, A.C.; Firestone, G.L.
Mol. Cell. Biol. 13, 2031-2040, 1993
A;Title: Characterization of sgk, a novel member of the serine/threonine protein kinase
A;Reference number: A48094; MUID:93204949; PMID:8455596
A;Accession: A48094
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-431 <WEB>
A;Experimental source: Con8.hdc mammary epithelial tumor cells
A;Note: sequence extracted from NCBI backbone (NCBIN:127618, NCBI:P:127619)
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol
C;Keywords: ATP
F;96-355/Domain: protein kinase homology <KIN>
F;104-112/Region: protein kinase ATP-binding motif

Query Match 90.5%; Score 2118; DB 2; Length 431;
Best Local Similarity 97.3%; Pred. No. 1.5e-87;
Matches 396; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 39 LAFWKQRMGLNDFIQKIANNYSACKHPEVQSILKISQPEPELMNANPPPPSPSQIN 98
Db 25 IAFWKQRMGLNDFIQKIANNYSACKHPEVQSILKISQPEPELMNANPPPPSPSQIN 84
Qy 99 LGPSSNPAPKPSDFHFLKVGKSGFVKVLLARHKAEEVFYAVKLVQKAILKKKEKHIM 158
Db 85 LGPSSNPAPKPSDFHFLKVGKSGFVKVLLARHKAEEVFYAVKLVQKAILKKKEKHIM 144
Qy 159 SERNVLLKNVKKHFLVGLHFSFQTADKLYFVDYINGGELFYHLQRECFLEPRARYAA 218
Db 145 SERNVLLKNVKKHFLVGLHFSFQTADKLYFVDYINGGELFYHLQRECFLEPRARYAA 204
Qy 219 EIASALGYLHSLNIVRDLPENILDSQGHIVLTFGLCKENIEHNSTSTFCGTPEYL 278
Db 205 EIASALGYLHSLNIVRDLPENILDSQGHIVLTFGLCKENIEHNSTSTFCGTPEYL 264
Qy 279 APVVLHKQPYDRTVDMWGLGAVLYEMLYGLPPFSYRNTAEYDNLNKLQKLNITNSA 338
Db 265 APVVLHKQPYDRTVDMWGLGAVLYEMLYGLPPFSYRNTAEYDNLNKLQKLNITNSA 324
Qy 339 RHLEGLLQKDRTKRLGAKDDFMFKSHVFFSLINWDDLINKKITPPFNPNVSGPDLRH 398
Db 325 RHLEGLLQKDRTKRLGAKDDFMFKSHVFFSLINWDDLINKKITPPFNPNVSGPDLRH 384
Qy 399 FDFEFTPEEPVNPISGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 445
Db 385 FDFEFTPEEPVNPISGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 431

RESULT 2

T26334
 Hypothetical protein W1066.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T26334
 R:McMurray, A.
 Submitted to the EMBL Data Library, October 1996
 A:Reference number: Z20201
 A:Accession: T26334
 A:Status: preliminary;
 A:Map position: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-422 <W1>
 A:Cross-references: EMBL:Z81140; PIDN:CA803485.1; GSPDB:GN00028; CESP:W1066.2
 A:Experimental source: clone W1066
 C:Genetics:
 A:Gene: CESP:W1066.2
 A:Map position: X
 A:Introns: 14/3; 60/2; 88/2; 135/3; 179/3; 217/2; 290/3; 393/1
 C:Superfamily: unassigned Ser/thr or Tyr-specific protein kinases; protein kinase homolo

Query Match 46.2%; Score 1082; DB 2; Length 422;
 Best Local Similarity 52.0%; Pred. No. 1.3e-41;
 Matches 204; Conservative 71; Mismatches 99; Indels 18; Gaps 4;
 Qy 32 ESFLSLGLAFMKQRMGLNDFIQKIANNVYACKHPEVQSILKISQPELMNANPSPPPP 91
 Db 29 KKFLQADSKFYEKRRVWILVISQHLVDNN--LRSEDVRRFFHLESPPDDE----- 76
 Qy 92 SPSQOINLGSSNPHAKPSDFHFKVIGKSGFGVLLARHKAEEVFYAVKVLQKATLKK 151
 Db 77 ---NNVDLGSERKTATANDFDYLTIGKSGFGVYQVRHKEKTKIYAMKILSKHEIRKK 133
 Qy 152 KEERHIMSERVLLKNNKVPGLVGLHFSFQADKLYFVLDYINGGELFYHLQRCFLEP 211
 Db 134 NEVKHVAERNVLNFKGFLPVLVSFQNKELFYVLDHLNGELFSLHQREKHS 193
 Qy 212 RARYAAEIASALGYLSNLNIVYRDLPENILLDSQGHIVLTDGLCKENIEHNSSTSTF 271
 Db 194 RSRYAAEIASALGYLHKEKNIYRDLPENILLDSQGHIVLTDGLCKEDMQGSKTSTF 253
 Qy 272 CGTEYLAPLHVKQPDRTVDWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLQK 331
 Db 254 CGTEYLAPLHVKQPDRTVDWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLQK 313
 Qy 332 PNITNSARHLLEGGLQKDRKRLGAKDDFMELIKSHVFFSLINWDDLINKKITPPFPNVS 391
 Db 314 HNISVPCSELITGLLQKDRSKRLGRNDRFDRHPPFLPVDWCKLNRELKAPFIPKVK 373
 Qy 392 GPNDRHFDPEFTEPEV-PNSIGKSPDSVLVT 422
 Db 374 NAMDTSNISKEFVEIQIDPSSL--APQQLAVT 403

RESULT 3

A59380
 protein kinase (EC 2.7.1.37) akt3 long splice form [similarity] - human
 N:Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific prote
 C:Species: Homo sapiens (man)
 C:Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 20-Apr-2001
 C:Accession: A59380; A59379
 R:Brodebeck, D.; Cron, P.; Hemmings, B.A.
 J. Biol. Chem. 274, 9133-9136, 1999
 A:Title: A human protein kinase Bgamma with regulatory phosphorylation sites in the acti
 A:Reference number: A59380; MUID:99194749; PMID:10092583
 A:Accession: A59380
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-479 <BRO>
 A:Cross-references: GB:AA23089; NID:94757579; PIDN:AA29089.1
 R:Maure, S.; Haefner, B.; Wesselsink, J.J.; Hoefnagel, E.; Mortier, E.; Verhasselt, P.;

Eur. J. Biochem. 265, 353-360, 1999
 A:Title: Molecular cloning, expression and characterization of the human serine/threoni
 A:Reference number: A59379; MUID:99421751; PMID:10491192
 A:Accession: A59379
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-479 <MAS>
 A:Cross-references: GB:CA853537; NID:95804886; PIDN:CA853537.1
 C:Genetics:
 A:Gene: GDB:AKT3; PRBG; PRKBG; RAC-gamma
 A:Cross-references: GDB:9954867
 A:Map position: 1q44-1q44
 C:Function:
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoni
 A:Pathway: signal transduction pathways regulating various processes
 C:Superfamily: protein kinase akt; pleckstrin repeat homology; protein kinase homology
 C:Keywords: ATP; autophosphorylation; phosphotransferase; phosphotransferase; proto-oncogen
 F:7-108/Domain: pleckstrin repeat homology <PLK>
 F:149-408/Domain: protein kinase homology <KIN>
 F:157-165/Region: protein kinase ATP-binding motif
 F:177/Active site: Lys #status predicted
 F:305/Binding site: phosphate (Thr) (covalent) #status predicted
 F:474/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predict
 Query Match 39.1%; Score 916; DB 1; Length 479;
 Best Local Similarity 45.1%; Pred. No. 3.5e-34;
 Matches 193; Conservative 67; Mismatches 140; Indels 28; Gaps 7;
 Qy 33 SFLSLGLAFMKQRMGLNDFIQK-----IANNVYACKHPE-----VQSILKISQPP 78
 Db 53 NFSVAKQLMKTERPKPNTFIIRCLQWTVTERTFHTDTPEREEMTEAQAADRLQK 112
 Qy 79 EPELMANPSPSPSQOINLG-----PSSNPHAK---PSDFELKVLKSGFGVLLARH 131
 Db 113 EBERMNCSP-----SQIDNIGEEEDASTTHKRKTMDNDFYLLKLGKGTFGKVLVRE 167
 Qy 132 KAEVFAVAVKVLQKATLKKKEKHIMSERVLLKNNKVPGLVGLHFSFQADKLYFVLD 191
 Db 168 KASKGYAMKILKEVIIAKDEVAHILTESRV-LKTRHFFLTLKYSFOTKDLFCWE 226
 Qy 192 YINGGELFYHLQRCFLEPRARYAAEIASALGYLSNLNIVYRDLPENILLDSQGHIV 251
 Db 227 YVNGGELFFHLRERFVSEDRTRFYGAIEVSALDYHSGKIVYRDLPENILLDSQGHIV 286
 Qy 252 LTDGLCKENIEHNSITSTECGTPEYLAPLHVKQPDRTVDWCLGAVLYEMLYGLPPF 311
 Db 287 ITDFGLCKEGITDAATMTKTCGTPEYLAPLHVKQPDRTVDWCLGAVLYEMLYGLPPF 346
 Qy 312 YSRNTAEYDNLNKPQLKPNITNSARHLLEGGLQKDRKRL-GAKDDFMELIKSHVFFS 370
 Db 347 YNODHEKLFELIMEDIKFPRTLLSSDAKSLGILLKDPNKLGGGPDDAKEIMRHSFFS 406
 Qy 371 LINWDDLKINKITPPFPNPNVSGPNDLRHFDPEFTEPEVPNSIGKSPDSVLTVASVKBAE 430
 Db 407 GVNWDVYDKLVPPFPKQVTSQTRFYDFDEFTAQITITTPPEKYDEDCMDNRRRP 466
 Qy 431 AFLGFSYA 438
 Db 467 HFPQFSYS 474
 RESULT 4
 T17287
 protein kinase (EC 2.7.1.37) akt3 short splice form - human
 N:Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific prot
 C:Species: Homo sapiens (man)
 C:Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 31-Mar-2001
 C:Accession: T17287
 R:Pouskka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, September 1999
 A:Reference number: T17287
 A:Accession: T17287
 A:Molecule type: mRNA

A;Residues: 1-462 <POU>
A;Cross-references: EMBL:AL117525; GB:CA55977; NID:G5912043; PIDN:CA55977.1
A;Experimental source: adult testis; clone DKF2p434N0250
R; Nakatani, K.; Thompson, D.A.; Barthel, A.; Sakaue, H.; Liu, W.; Weigel, R.J.; Roth, R.
J. Biol. Chem. 274, 21528-21532, 1999
A;Title: Up-regulation of Akt3 in estrogen receptor-deficient breast cancers and androgen
A;Reference number: A64199; PMID:10419456
A;Contents: annotation
A;Comment: This protein is increased in estrogen receptor-negative breast cancers and an
C;Genetics:
A;Gene: GDB:AKT3
A;Cross-references: GDB:9954867
A;Map position: 1q44-1q44
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A;Pathway: signal transduction pathways regulating various processes
C;Superfamily: protein kinase akt; pleckstrin repeat homology; protein kinase homology
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k
F;4-105/Domain: pleckstrin repeat homology <PLK>
F;146-405/Domain: protein kinase homology <PK>
F;154-162/Region: protein kinase ATP-binding motif
F;177/Active site: Lys #status predicted

Query Match 39.0%; Score 912; DB 1; Length 462;
Best Local Similarity 47.0%; Pred. No. 5.1e-34;
Matches 187; Conservative 63; Mismatches 120; Indels 28; Gaps 7;

QY 33 SFLLSLGLAFMKQRMGLNDFIQK-----IANNYSACKHPE-----VQSILKISQPO 78
Db 53 NFSVAKCOLMKTTERPKNTFIIRCLQWTTVIERTFHVDTPEEREWEATEIQAVADRLQ 112

QY 79 EPELMANPPSPSPSQINLG-----PSSNPHAK-----PSDFHLKVIKSGSFGKVLARH 131
Db 113 EERMNCSPT-----SQIDNIGEEEMDASTTHHKRTMNDFDYLLKLGKTFGKVLVRE 167

QY 132 KAEVEFYAVKVLQKAILKKKEKHIMSRNVLKNVHPFLVGLHFSQTADKLFLVLD 191
Db 168 KASGKYAMKILKEVIIIAKDEVAHTLTESRV-LKNTRHPFLTSLKYSFQTKDRLCFVME 226

QY 192 YINGGELFYHLQERCFLEPRARFYAAEIASALGYLHSLNIVYRDLPKPNILLDSQGHV 251
Db 227 YNGGELFFHLRSRVSFSDRTFYGAIEVSALDYLSHGKIVYRDLPKPNILLDSQGHV 286

QY 252 LTDFGLCKENIEHNSTTSCGTPEYLAPEVLHQPYDRTVDMWCLGAVLYEMLYGLPPF 311
Db 287 ITDFGLCKEGITDAATMKTFCGTPEYLAPEVLENDYGRAVDWGLGVVYEMWMMCGRLPF 346

QY 312 YSRNTAEWYDNLINKPLQKPNITNSARHLEGLLOKDRKRL-GAKDDFMEIKSHVFFS 370
Db 347 YNQDHEKFLIIMEDIKFPRTLSDDAKSLSLGLLKDPNKRLLGGGPDPAKEIMRHSFFS 406

QY 371 LINWDDLKINKITPPPNPNVSGNDLRHFDPEETEPV 408
Db 407 GVNWQVDYDKLVPPPKPQVTSSETDTRYDEEFTAQTI 444

RESULT 5
JC4345
protein kinase (EC 2.7.1.37) akt3 [validated] - rat
N;Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific prote
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 31-Mar-2001
C;Accession: JC4345
R;Konishi, H.; Kuroda, S.; Tanaka, M.; Matsuzaki, H.; Ono, Y.; Kameyama, K.; Haga, T.; K
Biochem. Biophys. Res. Commun. 216, 526-534, 1995
A;Title: Molecular cloning and characterization of a new member of the RAC protein kinase
e C subtypes and beta gamma subunits of G proteins.
A;Reference number: JC4345; MUID:96063640; PMID:7488143
A;Accession: JC4345
A;Molecule type: mRNA
A;Residues: 1-454 <KON>
A;Cross-references: DDBJ:D49836; NID:g1136777; PIDN:BAA08637.1; PID:g1401040
A;Experimental source: brain

C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A;Pathway: signal transduction pathways regulating various processes
C;Superfamily: protein kinase akt; pleckstrin repeat homology; protein kinase homology
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein
F;4-105/Domain: pleckstrin repeat homology <PLK>
F;146-405/Domain: protein kinase homology <PK>
F;154-162/Region: protein kinase ATP-binding motif
F;177/Active site: Lys #status predicted

Query Match 38.9%; Score 910; DB 1; Length 454;
Best Local Similarity 47.0%; Pred. No. 6.1e-34;
Matches 187; Conservative 63; Mismatches 120; Indels 28; Gaps 7;

QY 33 SFLLSLGLAFMKQRMGLNDFIQK-----IANNYSACKHPE-----VQSILKISQPO 78
Db 53 NFSVAKCOLMKTTERPKNTFIIRCLQWTTVIERTFHVDTPEEREWEATEIQAVADRLQ 112

QY 79 EPELMANPPSPSPSQINLG-----PSSNPHAK-----PSDFHLKVIKSGSFGKVLARH 131
Db 113 EERMNCSPT-----SQIDNIGEEEMDASTTHHKRTMNDFDYLLKLGKTFGKVLVRE 167

QY 132 KAEVEFYAVKVLQKAILKKKEKHIMSRNVLKNVHPFLVGLHFSQTADKLFLVLD 191
Db 168 KASGKYAMKILKEVIIIAKDEVAHTLTESRV-LKNTRHPFLTSLKYSFQTKDRLCFVME 226

QY 192 YINGGELFYHLQERCFLEPRARFYAAEIASALGYLHSLNIVYRDLPKPNILLDSQGHV 251
Db 227 YNGGELFFHLRSRVSFSDRTFYGAIEVSALDYLSHGKIVYRDLPKPNILLDSQGHV 286

QY 252 LTDFGLCKENIEHNSTTSCGTPEYLAPEVLHQPYDRTVDMWCLGAVLYEMLYGLPPF 311
Db 287 ITDFGLCKEGITDAATMKTFCGTPEYLAPEVLENDYGRAVDWGLGVVYEMWMMCGRLPF 346

QY 312 YSRNTAEWYDNLINKPLQKPNITNSARHLEGLLOKDRKRL-GAKDDFMEIKSHVFFS 370
Db 347 YNQDHEKFLIIMEDIKFPRTLSDDAKSLSLGLLKDPNKRLLGGGPDPAKEIMRHSFFS 406

QY 371 LINWDDLKINKITPPPNPNVSGNDLRHFDPEETEPV 408
Db 407 GVNWQVDYDKLVPPPKPQVTSSETDTRYDEEFTAQTI 444

RESULT 6
A55888
protein kinase (EC 2.7.1.37) akt [similarity] - fruit fly (Drosophila melanogaster)
N;Alternate names: protein kinase B; RAC-PK; serine/threonine-specific protein kinase B
C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2001
C;Accession: A55888
R;Andjelkovic, M.; Jones, P.F.; Grossniklaus, U.; Cron, P.; Schier, A.F.; Dick, M.; Bil;
J. Biol. Chem. 270, 4066-4075, 1995
A;Title: Developmental regulation of expression and activity of multiple forms of the D
A;Reference number: A55888; MUID:95181376; PMID:7876156
A;Accession: A55888
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-611 <AND>
A;Cross-references: GB:X83510
C;Genetics:
A;Gene: FlyBase:RacPK
A;Cross-references: FlyBase:FBgn0013324
A;Start codon: ACG
A;Introns: 261/3; 327/3; 457/3; 535/3; 584/3
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A;Pathway: signal transduction pathways regulating various processes
C;Superfamily: protein kinase akt; pleckstrin repeat homology; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphorotain; phosphotransferase; serine/threon
F;105-209/Domain: pleckstrin repeat homology <PLK>
F;264-523/Domain: protein kinase homology <PK>
F;272-280/Region: protein kinase ATP-binding motif
F;295/Active site: Lys #status predicted

F;423/Binding site: phosphate (Thr) (covalent) #status predicted
F;566/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 38.2%; Score 894; DB 1; Length 611;
Best Local Similarity 54.3%; Pred. No. 4.1e-33;
Matches 178; Conservative 45; Mismatches 99; Indels 6; Gaps 4;

QY 111 DFHFLKVIKSGSKVLLARHKAEEVFYAVKVLQKAILKKKEKHMSERNVLLKNVXH 170
DB 265 NFBEFLKVLGSGTGGKVLCKREKATAKAIKILKEVILIOKDEVAHFTTESRV-LKSTNH 323
QY 171 PFVLGLHFSQTDADKLYFVLDYINGGELFYHLQRECFLEPRARFYAAEIASALGYLHSL 230
DB 324 PFLISLKYSTQNDRLCFVQVYNGGELFWHLSHERIFTEDRFRFYCAEIIISALGYLHSG 363
QY 231 NIYVRDLKPNILDSOGHIVLDFGLCKENIEHNSTSTFCGTPEYLADEVLHKQPYDR 290
DB 384 GIIYRDLKLENLLDKDGHIKVADFGLECKEDITYGRTTKTCGTPEYLADEVLLDNDYQG 443
QY 291 TVDWMLGAVLYEMLYGLPFYSRNTAEMYNILNKLQKPNITNSARHLLGGLQKOR 350
DB 444 AVDMWGTGVVYEMICGRLPFFYNQDHEKLFELILMEEIRPRTLGPEAKSLLS 381
QY 351 TKRL-GAKDDFMETIKSHVFFSLNWDLLINKKITPPFNPNVSGPNDLHFDPEFTPEPVP 409
DB 504 KRLGGGKDDVKELOAHFFASINWTDVLKTKPPPPKQVTSDDTRYFDKFTGESVE 563
QY 410 NSIGKSPDSVLVTASVKEAAEAFLGFSY 437
DB 564 LT---PPDPTGPLGSIAE-EPLFPQFSY 587

RESULT 7

protein kinase (EC 2.7.1.37) akt1 [validated] - rat
N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prote
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 20-Apr-2001
C;Accession: J2437
R;Konishi, H.; Shinomura, T.; Kuroda, S.; Ono, Y.; Kikkawa, U.
Biochem. Biophys. Res. Commun. 205, 817-825, 1994
A;Title: Molecular cloning of rat RAC protein kinase alpha and beta and their associati
A;Reference number: J2437; MUID:95091823; PMID:7999118
A;Accession: J2437
A;Molecule type: mRNA
A;Residues: 1-480 <KON>
A;Cross-references: DDBJ:D30040; NID:9485402; PIDN:BA06279.1; PID:9485403
A;Experimental source: testis
C;Function:

A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A;Pathway: signal transduction pathways regulating various processes
C;Superfamily: protein kinase akt; pleckstrin repeat homology; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F;4-106/Domain: pleckstrin repeat homology <PLK>
F;148-408/Domain: protein kinase homology <KIN>
F;156-164/Region: protein kinase ATP-binding motif
F;179/Active site: Lys #status predicted
F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki
F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 37.5%; Score 878; DB 1; Length 480;
Best Local Similarity 41.9%; Pred. No. 1.7e-32;
Matches 191; Conservative 81; Mismatches 146; Indels 38; Gaps 10;

QY 18 RPR-----HKRAEAKRSES-----FLLSGLAFMKQRMGLNDFIQK----- 55
DB 23 RPRYFLKNDGDTFTGYKERPDVQDRESPLNFSVAQCQLMKTERPRPTFIIRCLQWTT 82
QY 56 IANNSYACKHPE-----VQSILKISQPEPELMNANSPPP--SPSQOINLGPSNP 105
DB 83 VIERTFHVETPEEREWEWTATQTVADGLKQKEETMDFRSGSPSDNSGAEEMEVAKPK 142
QY 106 H-AKPSDFHFLKVIKSGSKVLLARHKAEEVFYAVKVLQKAILKKKEKHMSERNVL 164

DB 143 HRVTWNEFEYKLGKGTGKVLVKEKATGRYYAMKILKKEIVAKDEVAHFTLTS-NRV 201
QY 165 LKNVGHFPFLVGLHFSQTDADKLYFVLDYINGGELFYHLQRECFLEPRARFYAAEIASAL 224
DB 202 LQNSRHPFLTALKYSQTDHRLCFVMEYANGGELFFHLSSRERVFSSDRARFYGAETVSAL 261
QY 225 GYLHS-LNIVYRDLKPNILDSOGHIVLDFGLCKENIEHNSTSTFCGTPEYLADEVL 283
DB 262 DYLHSEKNVYVYRDLKLENLMDKDGHIKITDFGLCKEGIKDGMTKTCGTPEYLADEVL 321
QY 284 HKQPYDRTYDWMLGAVLYEMLYGLPFYSRNTAEMYNILNKLQKPNITNSARHLL 343
DB 322 EDNDYGRAVDWMLGAVLYEMLYGLPFYSRNTAEMYNILNKLQKPNITNSARHLL 381
QY 344 GLLQKQRTKRL-GAKDDFMETIKSHVFFSLNWDLLINKKITPPFNPNVSGPNDLHFDPE 402
DB 382 GLLKKDPTQRLGGSGSDAKEIMQHRFFANIVMDVYEKLSPPFPKQVTSDDTRYFDEE 441
QY 403 FTEEPVNSIGKSPDSVLVTASVKEAAEAFLGFSYA 438
DB 442 FTAQMIIITPPDDDSMECVDS--ERRPHFPQFSY 475

RESULT 8

S33364

protein kinase (EC 2.7.1.37) akt1 [similarity] - mouse
N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prote
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Apr-2001
C;Accession: S33364
R;Bellacosa, A.; Franke, T.F.; Gonzalez-Portal, M.E.; Datta, K.; Taguchi, T.; Gardner,
Oncogene 8, 745-754, 1993
A;Title: Structure, expression and chromosomal mapping of c-akt: relationship to v-akt
A;Reference number: S33364; MUID:93173519; PMID:8437858
A;Accession: S33364
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-480 <BEL>
A;Cross-references: EMBL:X65687; NID:9287806; PIDN:CAA46620.1; PID:9287807
C;Genetics:

A;Gene: MGI:Akt
A;Cross-references: MGI:87986
A;Map position: 12
C;Function:

A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-throni
A;Pathway: signal transduction pathways regulating various processes
C;Superfamily: protein kinase akt; pleckstrin repeat homology; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogen
F;4-106/Domain: pleckstrin repeat homology <PLK>
F;148-408/Domain: protein kinase homology <KIN>
F;156-164/Region: protein kinase ATP-binding motif
F;179/Active site: Lys #status predicted
F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein k
F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predict

Query Match 37.5%; Score 878; DB 1; Length 480;
Best Local Similarity 41.9%; Pred. No. 1.7e-32;
Matches 194; Conservative 77; Mismatches 140; Indels 52; Gaps 11;

QY 18 RPR-----HKRAEAKRSES-----FLLSGLAFMKQRMGLNDFIQK----- 55
DB 23 RPRYFLKNDGDTFTGYKERPDVQDRESPLNFSVAQCQLMKTERPRPTFIIRCLQWTT 82
QY 56 IANNSYACKHPE-----VQSILKISQPEPELMNANSPPPSPS-----QQINLGPS 103
DB 83 VIERTFHVETPEEREWEWTATQTVADGLKQKEETMDFRSGSPSDNSGAEEMEVSL----- 138
QY 104 NPAKPE-----SDFHFLKVIKSGSKVLLARHKAEEVFYAVKVLQKAILKKKEKH 157
DB 139 ---AKPKRVTMNEFEYKLGKGTGKVLVKEKATGRYYAMKILKKEIVAKDEVAH 195
QY 158 MSERNVLLKNVGHFPFLVGLHFSQTDADKLYFVLDYINGGELFYHLQRECFLEPRARFYA 217

Qy	218	AETASALGYLHS-LNTIVYDLKPNENILLDSQGHIVLTDFGLCKENIEHNSTTSTFCGTPE	276
Db	538	AETVSALDYLSKENVVYRDCLKLENMLDKDGHIKITDFGLCKEGIKDGMATKMTFCGTPE	597
Qy	277	YLAPEVLHKQPYDRYTDVDMWCLGAVLYEMLYGLPPFSYRNTAEMYNILNKPLQLKPNITN	336
Db	598	YLAPEVLENDYGRAVDMWGLGVYMTVMCGRUPFYNQDHEKUFELILMBEIRFPRTGLP	657
Qy	337	SARHLLEGLLQKDRTKRL-CAKDDMFMEIKSHVFFSLINWDDLINKKITPPFNPNVSGPND	395
Db	658	EAKSLLSGLLKKDPTQRLGGSDAKEMIOHRRFANIVMQDVYEKKLSPFPKQVTSSETD	717
Qy	396	LRHFDDEFTPEEPVNSIGKSPDSVLVTASVKEAAEAPLGFPSYA	438
Db	718	TRYFDEBTAQMIIITPPDQDSMECVDS--ERRPHFPQPSYS	758

RESULT 10

A38578

protein kinase 2 (EC 2.7.1.1-) - slime mold (Dictyostelium discoideum)

C;Species: Dictyostelium discoideum

C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 24-Sep-1999

C;Accession: A38578

R;Haribabu, B.; Dottin, R.P.

R;Proc. Natl. Acad. Sci. U.S.A. 88, 1115-1119, 1991

A;Title: Identification of a protein kinase multigene family of Dictyostelium discoideum

A;Reference number: A38578; MUID:91142122; PMID:1996312

A;Accession: A38578

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-479 <GB>

A;Cross-references: NID:g167717; PIDN:AAA33186.1; PID:g167718

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol

C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threon

F;151-407/Domain: protein kinase homology <KIN>

F;159-167/Region: protein kinase ATP-binding motif

Query Match 36.9%; Score 864.5; DB 2; Length 479;

Best Local Similarity 48.5%; Pred. No. 6.7e-32;

Matches 183; Conservative 56; Mismatches 111; Indels 27; Gaps 8;

Qy	84	NANSPPPPPSGSQIN-----LGP-----SSNPHAKPSDFHFLKVIGKSGFKVLLARH	131
Db	113	NEASSSPDPSNGSGNGNDDEDEGEPEEVIFSPKKNQSATKDDFELLNVIGKSGFKVMQVK	172
Qy	132	KAEVYAVKVLQKAILKKKEKHIMSERNVLLKVKHPFLVGLHFSFOTADKLYEVL	191
Db	173	KGSDKIFAMKVLURKDAIIARKQVNHTKSEKTI-LQCISHPFIYNLHYAFOTKLYNVL	231
Qy	192	YINGGELFYHLQRCFCLEPRARFYAAETASALGYLHSLNIVYRDLKPNILLDSQGHIV	251
Db	232	FVNGGELFFHLKREGFSRPRVKIYAAEIVSALDHLHKQDIVYRDLKPNILLDSQGHIC	291
Qy	252	LTDGFLCKENIEHNSTTSTFCGTPEYLAPEVLHKQPYDRYTDVDMWCLGAVLYEMLYGLPPF	311
Db	292	ITDFGLSKK-IETDTGTFTCGTPEYLAPEVLNMGHGCAVDWWSLGLLLEYMLTGLPPF	350
Qy	312	YSRNTAEMYNILNKPLQKPNITNSARHLLEGLLQKDRTKRLGAKDDFMEIKSHVFFSL	371
Db	351	YSONVSTMTQKILINGELKPTYISPAKSLLEGLLTREVDRKRLGTGKG-GEVQHPMFKN	409
Qy	372	INWDDLINKKITPPFNPNVSGPNDLRHFPDTEEPVNSIGKSPDSVLVTASVKEAA--	429
Db	410	IDWEKLDREVEVHFHPKVKSGTDISQIDPVFTQE-----RPMDSLIVTSALGDAMGK	462
Qy	430	-EAPLGFSPAPPTDSEFL	445
Db	463	DTSEFGFTYV--ADSIL	477

RESULT 11

A46288

protein kinase (EC 2.7.1.37) akt2 - human

N;Alternate names: protein kinase B beta; RAC-PK-beta; serine/threonine-specific protein kinase
C;Species: Homo sapiens (man)
C;Date: 22-Sep-1993 #sequence_revision 12-May-1994 #text_change 31-Mar-2001
C;Accession: A46288
R;Cheng, J.Q.; Godwin, A.K.; Bellacosa, A.; Taguchi, T.; Franke, T.F.; Hamilton, T.C.; et al.
Proc. Natl. Acad. Sci. U.S.A. 89, 9267-9271, 1992
A;Title: AKT2, a putative oncogene encoding a member of a subfamily of protein-serine/threonine kinases
A;Reference number: A46288; MUID:93028445; PMID:1409633
A;Accession: A46288
A;Molecule type: mRNA
A;Residues: 1-481 <CHE>
A;Cross-references: GB:M95936; NID:g178325; PIDN:AAA58364.1; PID:g178326
A;Note: sequence extracted from NCBI backbone (NCBIP:115859)
C;Comment: This protein is amplified in some pancreatic, ovarian, and other carcinomas.
C;Genetics:
A;Gene: GDB:AKT2
A;Cross-references: GDB:135660; OMIM:164731
A;Map position: 19q13.2-19q13.2
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-phosphate
A;Pathway: signal transduction pathways regulating various processes
C;Superfamily: protein kinase akt; pleckstrin repeat homology; protein kinase homology
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase
F;4-106/Domain: pleckstrin repeat homology <PLK>
F;150-409/Domain: protein kinase homology <KIN>
F;158-166/Region: protein kinase ATP-binding motif
F;181/Active site: Lys #status predicted

Query Match 36.9%; Score 863.5; DB 1; Length 481;
Best Local Similarity 42.6%; Pred. No. 7.4e-32;
Matches 182; Conservative 70; Mismatches 138; Indels 37; Gaps 7;

QY 18 RPR-----HKRAEAQKRS-----ESLLSGLAFMKQRRMGLNDFIOK----- 55
DB 23 RPRYFLKDGSGFYGERPEADQTLPLNFSVAQCQLMKTERPRNPTFVIRCLQWTT 82
QY 56 IANNSYACKHPE-----VOSILKISQPEPELMANPSPPPSQOINLGPSSN 104
DB 83 VIERTFHVDSFDEREHWRAIQVANSKQRAQGEDPMYKCGSPDSSTTEMEVAVSK 142
QY 105 PHAK--PSDFHFLKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKKKEKHMSERN 162
DB 143 ARAKVTMNDPDLKLLGKGTGKVLVREKATGRYAMKILRKEVITAKDEVAHTVESR 202
QY 163 VLLKNVHPPLVGLHFSFQADKLYFVLDYINGGELFYHLQRCFLPEPRYAAEIAS 222
DB 203 V-LQNRHPLTALKYAFQTHDRLCFVMEYANGELFFHLRSRERVFTEERARYGAEIVS 261
QY 223 ALGYLHSLNIVYRDLKPEINLLDSQGHIVLTFGLCKENIEHNSTSTFCGTPEYLAPEV 282
DB 262 ALGYLHSLNIVYRDLKPEINLLDSQGHIVLTFGLCKENIEHNSTSTFCGTPEYLAPEV 321
QY 283 LHKQPYDRTYDVMWCLGAVLYEMLYGLPPFPYSRNTAEYDNLKPLQKNITNSARHLL 342
DB 322 LEDNDYGRAVDWMLGVVYEMMCGRLFPYVQDHERLFELILMEEIRFPRTLSPKSL 381
QY 343 EGLLOKDRTRL--GAKDDFMEIKSHVFFSLNMDLKNKITTFFPNPNVSGPNDLRHFD 401
DB 382 AGLLKDKPKRLGGGSDAKVEHREHRLFFLSINQDVVQKLLPPFPQVTSVDTRYFDD 441
QY 402 EFTPEEV 408
DB 442 EFTAQSI 448

RESULT 12
S62117
protein kinase (EC 2.7.1.37) akt1 [similarity] - bovine
N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific protein kinase
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 14-Dec-2001
C;Accession: S62117; S24423; S17999; S15714; S36388
R;Coffer, P.J.; Woodgett, J.R.

submitted to the EMBL Data Library, December 1991
A;Reference number: S62117
A;Accession: S62117
A;Molecule type: mRNA
A;Residues: 1-480 <COF>
A;Cross-references: EMBL:X61036; NID:g630; PIDN:CAA43371.1; PID:g631
A;Note: this is a revision to the sequence from reference S17999
R;Coffer, P.J.; Woodgett, J.R.
Eur. J. Biochem. 205, 1217, 1992
A;Reference number: S24423; MUID:92249329; PMID:1533586
A;Contents: erratum
A;Accession: S24423
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 70-78, N', 80-145 <COH>
A;Cross-references: EMBL:X61036
A;Note: this is a revision to the sequence from reference S17999
R;Coffer, P.J.; Woodgett, J.R.
Eur. J. Biochem. 201, 475-481, 1991
A;Title: Molecular cloning and characterisation of a novel putative protein-serine kinase
A;Reference number: S17999; MUID:92037600; PMID:1718748
A;Accession: S17999
A;Molecule type: mRNA
A;Residues: 1-70, 'TPSSAACSPPRSSARSSTWRPRSGVDHRRPDGGRRAQAGGDDGLFVGLTRRELGGRGDGVAGV
A;Cross-references: EMBL:X61036
A;Note: this sequence has been revised in references S62117 and S24423
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-phosphate
A;Pathway: signal transduction pathways regulating various processes
C;Superfamily: protein kinase akt; pleckstrin repeat homology; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogen
F;4-106/Domain: pleckstrin repeat homology <PLK>
F;148-408/Domain: protein kinase homology <KIN>
F;156-164/Region: protein kinase ATP-binding motif
F;179/Active site: Lys #status predicted
F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein kinase
F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 36.8%; Score 862; DB 1; Length 480;
Best Local Similarity 41.0%; Pred. No. 8.6e-32;
Matches 190; Conservative 80; Mismatches 141; Indels 52; Gaps 11;

QY 18 RPR-----HKRAEAQKRS-----FLLSGLAFMKQRRMGLNDFIOK----- 55
DB 23 RPRYFLKNDGTGFIGYKERPDLEQRESPLNFSVAQCQLMKTERPRNPTFIRCLQWTT 82
QY 56 IANNSYACKHPE-----VOSILKISQPEPELMANPSPPPSPS---QQINLGPSS 103
DB 83 VIERTFHVETPEEREBWTTAIQTVDGLKQREBETMDFRSGSPGNSGAEVSL---- 138
QY 104 NPAKP-----SDFHFLKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKKKEKHI 157
DB 139 ---AKPKHRVTWNEFEYVKKLGKGTGKVLVKEKATAAYYAMKILKEVIVAKDEVAHT 195
QY 158 MSERNVLLKNVHPPLVGLHFSFQADKLYFVLDYINGGELFYHLQRCFLPEPRARFYA 217
DB 196 LTF-NRVLQNSRHSITALKYSPQTHDRLCFVMEYANGELFFHLRSRERFVSDRARFYG 254
QY 218 AETASALGYLHS--LNTIVYRDLKPEINLLDSQGHIVLTFGLCKENIEHNSTSTFCGTPE 276
DB 255 AETVSALDYHSEKEVYVYRDLKLENLMDKDGHIKIDFGLCCKEGIKDGAATMTKTCGTPE 314
QY 277 YLAPEVLHKQPYDRTYDVMWCLGAVLYEMLYGLPPFPYSRNTAEYDNLKPLQKNITN 336
DB 315 YLAPEVLEDNDYGRAVDWMLGVVYEMMCGRLFPYVQDHERLFELILMEEIRFPRTLSP 374
QY 337 SARHLEGLLOKDRTRL--GAKDDFMEIKSHVFFSLNMDLKNKITTFFPNPNVSGPND 395
DB 375 EAKSLLSGLLKKDKPKRLGGGSDAKVEIMQHRFFASIVQDVYKELSLSPFPKQVTSSETD 434
QY 396 LRHFDPEFTPEEPVNSIGKSPSVLVTASVKEAAEAFLOFSYA 438
DB 435 TRYFDEEFTAQMITITPPQDDSDMEGVDSD--ERRPHFPQFSYS 475

RESULT 13.

A39360
 protein kinase (EC 2.7.1.37) akt1 [validated] - human
 N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific protein kinase
 C;Species: Homo sapiens (man)
 C;Date: 20-Mar-1992 #sequence_revision 12-May-1994 #text_change 30-Sep-2001
 C;Accession: A39360; S36389; S18000; S20836
 R;Jones, P.F.; Jakubowicz, T.; Picossi, F.J.; Maurer, F.; Hemmings, B.A.
 Proc. Natl. Acad. Sci. U.S.A. 88, 4171-4175, 1991
 A;Title: Molecular cloning and identification of a serine/threonine protein kinase of the human placenta
 A;Reference number: A39360; MUID:91239529; PMID:11851997
 A;Accession: A39360
 A;Molecule type: mRNA
 A;Residues: 1-480 <JON>
 A;Cross-references: GB:M63167; NID:G190827; PIDN:AAA36539.1; PID:G190828
 R;Coffer, P.J.; Woodgett, J.R.
 Eur. J. Biochem. 205, 1217, 1992
 A;Reference number: S24423; MUID:92249329; PMID:1533586
 A;Contents: extratumor
 A;Accession: S36389
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: mRNA
 A;Residues: 63-172, 'A', 175-201, 'Q', 203-211, 'R', 213-245, 'A', 247-408, 'T', 410-475, 'P', 477, 'P', 480-480
 A;Cross-references: EMBL:X61037; NID:G35480; PIDN:CAA43372.1; PID:G35481
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1991
 A;Note: this is a revision to the sequence from reference S17999
 R;Coffer, P.J.; Woodgett, J.R.
 Eur. J. Biochem. 201, 475-481, 1991
 A;Title: Molecular cloning and characterisation of a novel putative protein-serine kinase from the human placenta
 A;Reference number: S17999; MUID:92037600; PMID:1718748
 A;Accession: S18000
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 63-70, 'TPSSNAACGPISSNAPSWRLRSGGVNRRHPCGRRPQ', 'EAGGGDGLPVGLTORQLRGRDGGV' (63-70, 'TPSSNAACGPISSNAPSWRLRSGGVNRRHPCGRRPQ', 'EAGGGDGLPVGLTORQLRGRDGGV')
 A;Cross-references: EMBL:X61037
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1991
 A;Note: this sequence has been revised in reference S24423
 R;Coffer, P.
 submitted to the EMBL Data Library, July 1991
 A;Reference number: S20836
 A;Accession: S20836
 A;Molecule type: mRNA
 A;Residues: 63-70, 'TPSSNAACGPISSNAPSWRLRSGGVNRRHPCGRRPQ', 'EAGGGDGLPVGLTORQLRGRDGGV' (63-70, 'TPSSNAACGPISSNAPSWRLRSGGVNRRHPCGRRPQ', 'EAGGGDGLPVGLTORQLRGRDGGV')
 A;Cross-references: EMBL:X61037
 A;Note: this sequence has been revised in reference S24423
 R;Alessi, D.R.; Andjelkovic, M.; Caudwell, B.; Cron, P.; Morrice, N.; Cohen, P.; Hemming, B.A.
 EMBO J. 15, 6341-6551, 1996
 A;Title: Mechanism of activation of protein kinase B by insulin and IGF-1.
 A;Reference number: A64192; MUID:97133284; PMID:8978681
 A;Contents: annotation; phosphorylation sites
 R;Toker, A.; Newton, A.C.
 J. Biol. Chem. 275, 8271-8274, 2000
 A;Title: Akt/protein kinase B is regulated by autophosphorylation at the hypothetical phosphorylation sites
 A;Reference number: A64193; MUID:20187529; PMID:10722653
 A;Contents: annotation; autophosphorylation site
 C;Comment: Akt1 is ubiquitous as an inactive multimeric complex. It binds phosphatidylinositol (3,4,5)-trisphosphate and becomes fully active.
 C;Genetics:
 A;Gene: GDB:AKT1; RAC; PKB
 A;Cross-references: GDB:118989; OMIM:164730
 A;Map position: 14q32.32-14q32.32
 C;Function:
 A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-phosphate
 A;Pathway: signal transduction pathways regulating various processes including insulin resistance
 C;Superfamily: protein kinase akt; pleckstrin repeat homology; protein kinase homology
 C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
 F;4-106/Domain: pleckstrin repeat homology <PLK>
 F;148-408/Domain: protein kinase homology <KIN>
 F;156-164/Region: protein kinase ATP-binding motif
 F;179/Active site: Lys #status predicted

F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein kinase)
 F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status experiment
 Query Match 36.8%; Score 861; DB 1; Length 480;
 Best Local Similarity 42.3%; Pred. No. 9.6e-12;
 Matches 189; Conservative 76; Mismatches 144; Indels 38; Gaps 10;
 QY 18 RPRHKRAEAQKRSFLLSGLAFMKQRRMGLNDFIQK-----IANNYSACKHPE---- 67
 DB 41 RPQVDVQREAP--LNNFSAQCQLMKTERRPRPNTFIIRCLQWTVIERTFVETPEERE 98
 QY 68 ----VQSILKISQPOPELPMNPPSPSPS-----QQINLGPSSNPHAKP-----SDFH 113
 DB 99 WTTAIQTADVGLKKQBEEMDFRSGSPSDNSGAEMEVSLSL-----AKPKHRVTWNEFE 151
 QY 114 FLKVIKGGFGKVLARHKAEEVYAVKVLQKAILKKKEKHIMSGERNVLLKNVKKPFL 173
 DB 152 YLKLLKGGTGVKLVKKEATGRYAMKILKKEIVAKDEVAVHTLTET-NRVLQNSRRPFL 210
 QY 174 VGLHFSQTADKLYFVLDYINGGELFYHLQRCFLPRARFYAAEIASALGYLHS-LNI 232
 DB 211 TALKYSFQTHDRLCFVMEYANGGELFHLRSRVFSDRARFYGAIEVSALDYLHSEKNV 270
 QY 233 VYRDLKPENILLDSQGHIVLTDFGLCKENIEHNSSTSTFCGTPCYLAPEVLHKQPYDRTV 292
 DB 271 VYRDLKLENLMDKDHGHIKITDFGLCKEGIKDGTATMKTFCGTPCYLAPEVLEDNDYGRAV 330
 QY 293 DMWCLGAVLYEMLYGLPPFVSRNTAEYDNLKPLQKKNITNSARHLLGGLQKDRTK 352
 DB 331 DMWGLGVMYEMMCGRLPFYNGHEKLFELIMEEIRFPRTLGPKEAKLSUGLLKKDPKQ 390
 QY 353 RL-GAKDDFMEIKSHVFFSLINWDDLINKITPPFNPVNSGPNDRHDFEFTPEEPVNS 411
 DB 391 RLGGSGSDEAKEINQHRFFAGIVQHVYKLSPPFKPQVTSSETDTRFYDEEFTAQMITIT 450
 QY 412 IGKSPDSVLVTASVKAAEAFLGFSVA 438
 DB 451 PPQDDDSMECVDS--ERRPHFPQFSYS 475
 RESULT 14
 JC2438
 protein kinase (SC 2.7.1.37) akt2 [validated] - rat
 N;Alternate names: protein kinase B beta; RAC-PK-beta; serine/threonine-specific protein kinase
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 31-Mar-2001
 C;Accession: JC2438
 R;Konishi, H.; Shinomura, T.; Kuroda, S.; Ono, Y.; Kikkawa, U.
 Biochem. Biophys. Res. Commun. 205, 817-825, 1994
 A;Title: Molecular cloning of rat RAC protein kinase alpha and beta and their association with phosphoinositide 3-kinase
 A;Reference number: JC2437; MUID:95091823; PMID:7999118
 A;Accession: JC2438
 A;Molecule type: mRNA
 A;Residues: 1-481 <KON>
 A;Cross-references: DDBJ:D330041; NID:G485404; PIDN:BAA06280.1; PID:G485405
 A;Experimental source: testis
 C;Function:
 A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-phosphate
 A;Pathway: signal transduction pathways regulating various processes including myoblast differentiation
 C;Superfamily: protein kinase akt; pleckstrin repeat homology; protein kinase homology
 C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase
 F;4-106/Domain: pleckstrin repeat homology <PLK>
 F;150-409/Domain: protein kinase homology <KIN>
 F;158-166/Region: protein kinase ATP-binding motif
 F;181/Active site: Lys #status predicted
 Query Match 36.4%; Score 852.5; DB 1; Length 481;
 Best Local Similarity 42.2%; Pred. No. 2.3e-31;
 Matches 180; Conservative 71; Mismatches 139; Indels 37; Gaps 7;
 QY 18 RPR-----HKRAEAQKRS-----ESPLSGLAFMKQRRMGLNDFIQK----- 55
 DB 23 RPRYFLKSGDSFGYKERPEAPDOTLPLNNSVAECQLMKTERPRNTFVIRCLQWTT 82

```

- QY 56 IANNYSACKHPE-----VQSILKISQOPELPMNANPSPPPSPSQOINLGPSSN 104
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 VIERTFHVDFDEREEWIRAIQWVANSKQRGCEADAMDKCGSPSSDSSEMMVEAVSK 142
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 105 PHAK--PSDFHFLVICKGSGFKVLLARHKAEEVFYAVKVLQKAILKKKEKHIMSEIN 162
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 143 ARAKVTWMDFDYLLKLGKGTGKVLVREKATGRYYAMKILRKEVIIAKDEVAHTVESR 202
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 163 VLLKNVGHPELVGLHFSQFADKLYFVLVDYINGGELFYHLQRCFLEPRARYAAEIAS 222
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 203 V-LQNTRHPEFLTALKYAFQTHDLRCFYMEYANGDLFFHLRSERVFTEDEARYGAEIVS 261
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 223 ALGYLHSLNIVYRDLKPENILDSQGHIVLTDGFLCKENIEHNSSTTFCGTPEYLAPEV 282
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 262 ALEYLHSTDVVYRDIKLENLMDKXGHIKITDFGLSKEGSDGATMKTFCTGTEYLAPEV 321
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 283 LHKQPYDRTVDWMCGLAVLYEMLYGLPPFYSRNTAEYDNLNKPQLKKNITNSARHLL 342
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 322 LEDNDYGRAVDWGLGVVYEMMCGRLPFYQNDHERLFELILMBEIRFRTLGPKEAKSL 381
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 343 EGLLOKDRTKRL-GAKDDFWEIKSHVFFSLINWDDLLINKKITPPFPNPNVSGPNDLRHFD 401
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 382 AGLLKDKPKORLGGPSDAKEVMEHREFLSINQDVQVKLLPFPKQVTSVDTRYFDD 441
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 402 EFTPEPV 408
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 442 EFTAQSI 448
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
JS0178
protein kinase YKR2 (EC 2.7.1.1) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YMR104c; protein YMR104c
C;Species: Saccharomyces cerevisiae
C;Date: 07-Jun-1990 #sequence revision 07-Jun-1990 #text_change 24-Sep-1999
C;Accession: JS0178; S30904; S54565
R;Kubo, K.; Ohno, S.; Matsumoto, S.; Yahara, I.; Suzuki, K.
Gene 76, 177-180, 1989
A;Title: A novel yeast gene coding for a putative protein kinase.
A;Reference number: JS0178; MUID:89306654; PMID:2663649
A;Accession: JS0178
A;Molecule type: DNA
A;Residues: 1-677 <KUB>
A;Cross-references: EMBL:M24929; NID:g295680; PIDN:AAA78259.1; PID:g295681
R;Chen, P.; Lee, K.S.; Levin, D.E.
Mol. Gen. Genet. 236, 443-447, 1993
A;Title: A pair of putative protein kinase genes (YPK1 and YPK2) is required for cell growth.
A;Reference number: S30903; MUID:93173125; PMID:8437590
A;Accession: S30904
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-677 <CHE>
R;Hunt, S.; Bowman, S.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54510
A;Accession: S54565
A;Molecule type: DNA
A;Residues: 1-677 <HUN>
A;Cross-references: EMBL:Z49702; NID:g817859; PIDN:CAA89740.1; PID:g817862; MIPS:YMR104c
A;Experimental source: strain AB972
C;Genetics:
A;Gene: SGD:YKR2
A;Cross-references: SGD:S0004710; MIPS:YMR104c
A;Map position: 13R
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;35-57/Region: histidine-rich
F;342-599/Domain: protein kinase homology <KIN>
F;350-358/Region: protein kinase ATP-binding motif
F;351-375/Region: ATP binding #status predicted
F;466-512/Region: catalytic #status predicted

```

```

Query Match 35.5%; Score 831.5; DB 2; Length 677;
Best Local Similarity 43.5%; Pred. No. 2.6e-30;
Matches 193; Conservative 58; Mismatches 140; Indels 53; Gaps 9;

QY 11 ARLESLLRPHKRAAQAQRSEFLLSLGAFMKQRMGNDLNDFIQKIANNYSACKHPEVQS 70
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 253 ARIPSLLLPSKMQQIGQDEV-----LKEILKKINTN-----QD 288
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 71 I-----LKISQOPELPMNANPSPPPSPSQOINL-----GPSNPHAKPSDFHFLK 116
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 289 IHLDSFHLPLNLKIDSAQIRLYNHHWISLERGYGKLNITVDYKPKNKPPLSTDDFDLLK 348
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 117 VICKGSFGKVLARHKAEEVFYAVKVLQKAILKKKEKHIMSEINVLKNVHPELVGL 176
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 349 VICKGSFGKVMQVRKDTQKIYALKALRKAYIVSKCEVTHTLAERTVLAR-VDCPFIVPL 407
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 177 HFSFQTADKLYFVLVDYINGGELFYHLQRCFLEPRARYAAEIASALGYLHSLNIVYRD 236
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 408 KFSFQSPEKLYLVLAFLINGGELFYHLQHEGRFSLARSFYIAELLCALDSLHKLDVIYRD 467
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 237 LKPENILDSQGHIVLTDGFLCKENIEHNSSTTFCGTPEYLAPEVLHKKQPYDRTVDWMC 296
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 468 LKPENILLDYQGHIALCDFGLCKLNKMDNDTDFCGTPEYLAPEILLGGQYTKTVDMWT 527
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 297 LGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLKKNITNSARHLLLEGLLQKDRTKRLGA 356
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 528 LGILLYEMMTGLPPYDENVVPMYKKILOQPLLFPDGFDPAAKDLJLGLLSRDPSSRLGV 587
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 357 KDDFMEIKSHVFFSLINWDDLLINKKITPPFPNPNVSGPNDLRHFDPEFTPEVPNSIGKSP 416
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 588 -NGTDEIRNHPFFKQISWKLLKGVIPYKPIVKSEIDTANFDQBFTE-----KPI 639
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 417 DSVL-----VTASVKEAAEAFEGSY 437
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 640 DSVVDEYLSASIQ---KQFGGWTY 660

Search completed: June 20, 2003, 19:27:35
Job time : 44 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2003, 19:26:53 ; Search time 51 Seconds
(without alignments)
944.157 Million cell updates/sec

Title: US-10-067-977-2

Perfect score: 2340

Sequence: 1 MGEMOALARARLESLLRPR.....KEAAEAFLGFSVAPPTDSFL 445

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pap.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pap.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pap.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pap.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pap.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pap.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pap.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pap.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW PUB.pap.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pap.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW PUB.pap.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pap.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW PUB.pap.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2154	92.1	431	9	US-09-981-353-7
2	2150	91.9	431	9	US-10-000-039-2
3	2146	91.7	431	10	US-09-810-808-5
4	2100.5	89.8	430	10	US-09-810-808-9
5	1481	63.3	496	10	US-09-784-249-2
6	1411	60.3	367	10	US-09-971-118-2
7	968.5	41.4	276	9	US-09-764-868-669
8	916	39.1	479	10	US-09-771-161A-246
9	916	39.1	479	10	US-09-771-161A-247
10	916	39.1	479	10	US-09-771-161A-248
11	912	39.0	465	9	US-09-526-043-2
12	910	38.9	454	9	US-09-526-043-17
13	889	38.9	321	9	US-10-116-722A-4
14	863.5	36.9	480	9	US-09-526-043-13
15	861.5	36.8	726	9	US-10-072-036-71
16	861	36.8	480	9	US-10-059-585-39
17	861	36.8	480	9	US-09-526-043-14
18	861	36.8	480	10	US-09-771-161A-223
19	861	36.8	480	10	US-09-970-000-4

20	861	36.8	492	9	US-09-955-999-96	Sequence 96, Appl
21	861	36.8	727	9	US-10-072-036-139	Sequence 139, App
22	845	36.1	319	9	US-10-116-722A-8	Sequence 8, Appli
23	843.5	36.0	320	9	US-10-116-722A-5	Sequence 5, Appli
24	842	36.0	319	9	US-10-116-722A-6	Sequence 6, Appli
25	838	35.8	480	10	US-09-205-658-157	Sequence 157, App
26	829.5	35.4	320	9	US-10-116-722A-7	Sequence 7, Appli
27	814	34.8	546	10	US-09-205-658-155	Sequence 155, App
28	801.5	34.3	541	10	US-09-205-658-154	Sequence 154, App
29	791.5	33.8	672	8	US-08-681-219-29	Sequence 29, Appl
30	787	33.6	322	9	US-10-116-722A-2	Sequence 2, Appli
31	784	33.5	637	10	US-09-817-310-2	Sequence 2, Appli
32	780.5	33.4	916	9	US-10-072-036-73	Sequence 73, Appl
33	778.5	33.3	737	9	US-10-228-931-4	Sequence 4, Appli
34	776	33.2	737	10	US-09-771-161A-195	Sequence 195, App
35	774.5	33.1	587	9	US-10-097-340-256	Sequence 256, App
36	758.5	32.4	584	10	US-09-842-307-2	Sequence 2, Appli
37	746	31.9	483	10	US-09-205-658-156	Sequence 156, App
38	742.5	31.7	740	10	US-09-771-161A-265	Sequence 265, App
39	742.5	31.7	740	10	US-09-771-161A-266	Sequence 266, App
40	742	31.7	311	9	US-10-116-722A-3	Sequence 3, Appli
41	732.5	31.3	824	10	US-09-801-368-312	Sequence 312, App
42	729.5	31.2	375	9	US-10-116-722A-1	Sequence 1, Appli
43	723	30.9	140	10	US-09-925-300-1800	Sequence 1800, Ap
44	714	30.5	584	9	US-10-029-903-10	Sequence 10, Appl
45	713.5	30.5	194	10	US-09-784-249-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-981-353-7
; Sequence 7, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 3819039CD1
US-09-981-353-7

Query Match	92.1%;	Score 2154;	DB 9;	Length 431;
Best Local Similarity	99.8%;	Pred. No. 1.8e-145;		
Matches 406;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	39	LAFMKQRRMGLNDFIOKIANNVYACHPEVQSTLKISQOPELMMANPSPSPSQOIN	98	
Db	25	IAPMKQRRMGLNDFIOKIANNVYACHPEVQSTLKISQOPELMMANPSPSPSQOIN	84	
QY	99	LQFSSNPHAKPSDFHFLKVGKSGFKVLLARHKAEEVFYAVKVLQKAILKKKEKHIM	159	
Db	85	LQFSSNPHAKPSDFHFLKVGKSGFKVLLARHKAEEVFYAVKVLQKAILKKKEKHIM	144	
QY	159	SERNVLLKNNKVPFLVGLHFSFQTADKLYFVDLYNGGELFYHLQRCERCELEPRARFYAA	218	
Db	145	SERNVLLKNNKVPFLVGLHFSFQTADKLYFVDLYNGGELFYHLQRCERCELEPRARFYAA	204	
QY	219	ETASALGYLHSLNIVYRDLKPENILDSQGHVLTDFGLCKENIEHNSTTSTFCGTPEYL	278	
Db	205	ETASALGYLHSLNIVYRDLKPENILDSQGHVLTDFGLCKENIEHNSTTSTFCGTPEYL	264	

QY 279 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPLQLKPNITNSA 338
 DB 265 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPLQLKPNITNSA 324
 QY 339 RHLLEGLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNVSGPNDLRH 398
 DB 325 RHLLEGLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNVSGPNDLRH 384
 QY 399 FDPEFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 445
 DB 385 FDPEFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 431

RESULT 2

US-10-000-039-2
 ; Sequence 2, Application US/10000039
 ; Publication No. US20030003559A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WALDEGGER, Florian
 ; TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FOLEY & LARDNER
 ; STREET: 3000 K Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/000.039
 ; FILING DATE: 04-Dec-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/031.295
 ; FILING DATE: 26-FEB-1998
 ; APPLICATION NUMBER: DE 197-08-173.8
 ; FILING DATE: 28-FEB-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sandercock, Colin G.
 ; REGISTRATION NUMBER: 31.298
 ; REFERENCE/DOCKET NUMBER: 058315/0123
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 672-5300
 ; TELEFAX: (202) 672-5399
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 431 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-000-039-2

Query Match 91.9%; Score 2150; DB 9; Length 431;
 Best Local Similarity 99.5%; Pred. No. 3.4e-145;
 Matches 405; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 39 LAFMKQRMGLNDFIQIANNYSACKHPEVQSIKISQPELNMNANPPSPSQOIN 98
 DB 25 IAFMKQRMGLNDFIQIANNYSACKHPEVQSIKISQPELNMNANPPSPSQOIN 84
 QY 99 LQSSNPHAKSPDFHLKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKKKEKHIM 158
 DB 85 LQSSNPHAKSPDFHLKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKKKEKHIM 144
 QY 159 SERNVLLKNVHPLVLGHLHFSQTADKLYFVLVDYINGELFYHLQRCFCLEPRARFYAA 218

DB 145 SERNVLLKNVHPLVLGHLHFSQTADKLYFVLVDYINGELFYHLQRCFCLEPRARFYAA 204
 QY 219 ETASALGYLHSLNIVYRDLKPENILLDGSGHIVLTDGGLCKENIEHNSTTSTFCGTPEYL 278
 DB 205 ETASALGYLHSLNIVYRDLKPENILLDGSGHIVLTDGGLCKENIEHNSTTSTFCGTPEYL 264
 QY 279 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPLQLKPNITNSA 338
 DB 265 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPLQLKPNITNSA 324
 QY 339 RHLLEGLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNVSGPNDLRH 398
 DB 325 RHLLEGLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNVSGPNDLRH 384
 QY 399 FDPEFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 445
 DB 385 FDPEFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 431

RESULT 3

US-09-810-808-5
 ; Sequence 5, Application US/09810808
 ; Patent No. US20020042114A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Au-Young, Janice
 ; Guegler, Karl J.
 ; Hawkins, Phillip R.
 ; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: U.S.
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/810.808
 ; FILING DATE: 15-Mar-2001
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/541,228
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0118 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 431 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; IMMEDIATE SOURCE:
 ; LIBRARY: <Unknown>
 ; CLONE: Consensus
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 US-09-810-808-5

Query Match 91.7%; Score 2146; DB 10; Length 431;
 Best Local Similarity 99.5%; Pred. No. 6.6e-145;
 Matches 405; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 39 LAFMKQRMGLNDFIQIANNYSACKHPEVQSIKISQPELNMNANPPSPSQOIN 98

25	Db	I A F M Q R R M G L N D F L Q K T A N N S Y A C K I P E V Q S I L K I S O P Q E P E L M N A N F S P P P S Q Q I N	84
99	Qy	L G P S S N H A K P S D P H F L K V I G K S F G V K L L A R H K A E E V F Y A V K V L Q K A I L K K K E E K H I M	158
85	Db	L G P S S N H A K P S D P H F L K V I G K S F G V K L L A R H K A E E V F Y A V K V L Q K A I L K K K E E K H I M	144
159	Qy	S E R N V L L K N V K H P F L V G L H F S F Q T A D K L Y F V L D Y I N G G E L F Y H L Q R E R C F L P R A R F Y A A	218
145	Db	S E R N V L L K N V K H P F L V G L H F S F Q T A D K L Y F V L D Y I N G G E L F Y H L Q R E R C F L P R A R S Y A A	204
219	Qy	E T A S A L G Y L H S I N I Y R D L K P E N I L L D S Q G H I V L T D F G L C K E N I E H N S T T S F C G T P E Y L	278
205	Db	E T A S A L G Y L H S I N I Y R D L K P E N I L L D S Q G H I V L T D F G L C K E N I E H N S T T S F C G T P E Y L	264
279	Qy	A P E V L H K O P Y D R T V D W M C L G A V L Y E M L Y G L P P F Y S R N T A E M Y N I L N K P L Q L K P N I T N S A	338
265	Db	A P E V L H K O P Y D R T V D W M C L G A V L Y E M L Y G L P P F Y S R N T A E M Y N I L N K P L Q L K P N I T N S A	324
339	Qy	R H L E G L L Q K O R T K E L G A K D D F M E I K S H V F F S L I N W D D L I N K K I T P P F P N V S G P N D L R H	398
325	Db	R H L E G L L Q K O R T K E L G A K D D F M E I K S H V F F S L I N W D D L I N K K I T P P F P N V S G P N D L R H	384
399	Qy	F D P E T E B P V N S I G K S P D S V L V T A S V K E A E A F L G F S Y A P P T D S F L	445
385	Db	F D P E T E B P V N S I G K S P D S V L V T A S V K E A E A F L G F S Y A P P T D S F L	431

RESULT 4

```

US-09-810-808-9
; Sequence 9, Application US/09810808
; Patent No. US20020042114A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
;           Guegler, Karl J.
;           Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/810,808
; FILING DATE: 15-Mar-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/541,228
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0118 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 430 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 294637
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:

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US-09-810-808-9

Query Match.	89.88;	Score	2100.5;	DB	10;	Length	430;
Best Local Similarity	97.18;	Pred. No.	1.1e-141;				
Matches	395;	Conservative	7;	Mismatches	4;	Indels	1;
Gaps	1;						
Qy	39	LAFWKQRRMGLNDF	IOKIANN	SACKHPEVQSIL	KISQOPE	PELMNANP	PPPPSQOIN
Db	25	IAPWKQRRMGLNDF	IOKLANN	SACKHPEVQSIL	KISQOPE	PELMNANP	PPPPSQOIN
Qy	99	LPSSNPHAKPSP	FHFLKV	ITGKSG	FGKVL	LAARHKA	BEVYAVK
Db	85	LPSSNPHAKPSP	FHFLKV	ITGKSG	FGKVL	LAARHKA	BEAFYAVK
Qy	159	SERNVLLKNVKH	PFLVGL	HFSP	OTADK	LYFVL	YDINGGEL
Db	145	SERNVLLKNVKH	PFLVGL	HFSP	OTADK	LYFVL	YDINGGEL
Qy	219	EIASALGYLHSL	NI	VYRDLK	PENIL	LD	SQGHIV
Db	205	EIASALGYLHSL	NI	VYRDLK	PENIL	LD	SQGHIV
Qy	279	APEVLHKQP	YDRTVD	WWCLG	AVLYE	MLYGL	PPPSYRNTA
Db	265	APEVLHKQP	YDRTVD	WWCLG	AVLYE	MLYGL	PPPSYRNTA
Qy	339	RHLLEGLLQ	KDRTKRL	CGAKDD	DFMEIK	SHVFFS	LI
Db	324	RHLLEGLLQ	KDRTKRL	CGAKDD	DFMEIK	SHIIF	LI
Qy	399	FDPEFTTEEP	VPNSIG	KSPDS	VLVTAS	VKEAAEA	FLGFSY
Db	384	FDPEFTTEEP	VPNSIG	RSPDS	ILVTAS	VKEAAEA	FLGFSY

RESULT 5

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US-09-784-249-2
; Sequence 2, Application US/09784249
; Patent No. US20010027184A1
; GENERAL INFORMATION:
; APPLICANT: Sanjay Kumar
; APPLICANT: Cheng Zou
; TITLE OF INVENTION: SERINE/THREONINE PROTEIN KINASE (H-SGK2)
; FILE REFERENCE: GH-70124-C1
; CURRENT APPLICATION NUMBER: US/09/784,249
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 08/997,212
; PRIOR FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: 60/051,446
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-784-249-2

Query Match      63.3%; Score 1481; DB 10; Length 496;
Best Local Similarity 67.7%; Pred. No. 1.4e-97;
Matches 281; Conservative 52; Mismatches 68; Indels 14; Gaps 3;

Qy      41  FMKQRMGLNDFIQKIANNYSACKHPVEQSIILKISPOEPELNANFSPPP----- 91
Db      86  FIKQRAGLNEFIQNLRYPELYKHPDVPRAFLQNDSPGH-----QSDSEDEKSSOKLH 141
Qy      92  SPSQQINLGPSNNPHAKPSDFHLKVIKGSGFGVLLARHKABEEVFYAVKVLQKAILKK 151
Db      142  STSQINILGPSGNPHAKPTDFDLKVIKGSGFGCKVLLAKRKLDGKFFAVKVLQKIVLNR 201
Qy      152  KEEKHIMSERNVLLKNVYKHPFLVGLHPSFOTAKLYFVLVDYINGGELFYHLQRERCFLEP 211
Db      202  KEOKHIMAEENVLLKNVYKHPFLVGLHYSFOTTEKLYFVLDFVNGGELFFHLQRERSPEH 261

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QY 212 RARYAAEIASALGYLHSLNIVYRDLPENILDSQGHIVLTDPLGCKENIEHNSTTSTF 271
Db 262 RARYAAEIASALGYLHSLNIVYRDLPENILDSQGHIVLTDPLGCKEGIAISDTTTF 321
QY 272 CGTPEYLAPEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKLQK 331
Db 322 CGTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMYNILHKLPLSR 381
QY 332 PNITNSARHLEGLLOKQDKRGLGAKDDFMEIKSHVFFSILNWDLLINKKITPPFPNVS 391
Db 382 PGVSLTAWSLIEELLELDKQNRILGAKEDFLEIQNHPPFESLWADLVQKKIPPPFPNVA 441
QY 392 GPNDLRFDFEETPEEPVNSIGKSPDSVLTASVKEAAEAFGLGFSYAPPT-DSFL 445
Db 442 GPDIRNFDTAFTETVPYSCVSSDYSIVNASVLEADDAFVGFYAPPSSEDLPL 496

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RESULT 6

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US-09-971-118-2
; Sequence 2, Application US/09971118
; Patent No. US20020123056A1
; GENERAL INFORMATION:
; APPLICANT: DELANEY, ALLEN
; TITLE OF INVENTION: THILAINATHAN
; FILE REFERENCE: KINE025CIP
; CURRENT APPLICATION NUMBER: US/09/971.118
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/21479
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/237,419
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-971-118-2

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Query Match 60.3%; Score 1411; DB 10; Length 367;
Best Local Similarity 71.2%; Pred. No. 9.4e-93;
Matches 262; Conservative 53; Mismatches 45; Indels 8; Gaps 3;

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QY 83 MNAMP--SPPPSPSQ---QINLGPSSNPHAKPSDFHLKVIKGSFKVLLARHKAEEVF 137
Db 1 MNSSPACTPSPQSRANGINLGPANPNAQPTDFDLKVIKGNVGVLLAKRKSDF 60
QY 138 YAVKVLQKATLKKKEKHIMSERNVLLKNVGHFPLVGLHFSFOTADKLYFVLVDYNGGE 197
Db 61 YAVKVLQKSLTKKKEQSHMAERSVLLKNVRHFPFLVGLRYSFOTPEKLYFVLVDYNGGE 120
QY 198 LFYHLQRCFLPEPRARYAAEIASALGYLHSLNIVYRDLPENILDSQGHIVLTDPL 257
Db 121 LFYHLQRCFLPEPRARYAAEIASALGYLHSLNIVYRDLPENILDSQGHIVLTDPL 180
QY 258 CKENIEHNSTSTFCGTPEYLAPEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTA 317
Db 181 CKGEVEPEDTTSTFCGTPEYLAPEVLKPEYDRAVDWCLGAVLYEMLYGLPPFYSQDVS 240
QY 318 EMDYNILNKLPLQKPNITNSARHLEGLLOKDKRGLGAKDDFMEIKSHVFFSILNWDLL 377
Db 241 QMYENILHQPQIPGGRTVACDDLLQSLHKKQQRGLGSKADFLKIHVFFSPINWDDL 300
QY 378 INKKITPPFPNVPNSGPNDRHDFEETPEEPVNSIGKSPDSVLTASVKEAAEAFGLGFSY 437
Db 301 YHKELTPFPNVPNTGADLKHDFEETPEEPVNSIGKSPDSVLTASVKEAAEAFGLGFSY 357
QY 438 APPTDSFL 445
Db 358 APEDDDIL 365

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RESULT 7

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US-09-764-868-669
; Sequence 669, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN ET AL.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION DATA REMOVED - REFER TO PALM OR FILE WRAPPER
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 669
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (17)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (181)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (233)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (254)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-868-669

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Query Match 41.4%; Score 968.5; DB 9; Length 276;

Best Local Similarity 70.9%; Pred. No. 1.9e-61;

Matches 180; Conservative 31; Mismatches 42; Indels 1; Gaps 1;

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QY 193 INGGELFYHLQRCFLPEPRARYAAEIASALGYLHSLNIVYRDLPENILDSQGHIVL 252
Db 23 VNGGELFYHLQRCFLPEPRARYAAEIASALGYLHSLNIVYRDLPENILDSQGHIVL 82
QY 253 TDFGLCKENIEHNSTSTFCGTPEYLAPEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFY 312
Db 83 TDFGLCKEGIAISDTTTFCTGTPEYLAPEVIRKQPYDNTVDMWCLGAVLYEMLYGLPPFY 142
QY 313 SRNTAEMYNILNKLPLQKPNITNSARHLEGLLOKDKRGLGAKDDFMEIKSHVFFSLI 372
Db 143 CRDVAEMYNILHKLPLSRPGVSLTASVLEELLELDKXNRILGAKEDFLEIQNHPPFESL 202
QY 373 NWDDLINKKITPPFPNVPNSGPNDRHDFEETPEEPVNSIGKSPDSVLTASVKEAAEAF 432
Db 203 SWADLVQKKIPPPFPNVPNAGPDDIRNFDTAFTETVPYSCVSSDYSIVNASVLEADDAF 262
QY 433 LGFSYAPPT-DSFL 445
Db 263 VGFSYAPPSSEDLPL 276

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RESULT 8

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US-09-771-161A-246
; Sequence 246, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619

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Qy	79	EPELNNANPSPPPSPSQINLG-----PSNPHAK--PSSDFHFLKVIHGSGCKVLLARH
Db	113	EEERNCSPT-----SQIDNIGEEEMDASTTHHKRTWNDDPYLKULGKGTFGKVILVRE
Qy	132	KAEVFYAVVKLQKAILKKKEEKHIMSEBRYNVLNKNVRHPPLVGUHFSPQTADKLXFVLD
Db	168	KASGYKYAMTKLKKVEVIAKDEVAHTLTESRV-LKNTRHFPFITSUKYSFQTKDLRCFGVME

RESULT 13
US-10-116-722A-4
; Sequence 4, Application US/10116722A
; Publication No. US20030044946A1
; GENERAL INFORMATION:
; APPLICANT: LONGO, VALTER D.
; TITLE OF INVENTION: GENES, MUTATIONS, AND DRUGS THAT INCREASE CELLULAR
; TITLE OF INVENTION: RESISTANCE TO DAMAGE AND EXTEND LONGEVITY IN ORGANISMS
; TITLE OF INVENTION: FROM YEAST TO HUMANS
; FILE REFERENCE: 13761-7068

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2003, 19:23:23 ; Search time 27 Seconds
(without alignments)
484.933 Million cell updates/sec

Title: US-10-067-977-2
Perfect score: 2340
Sequence: 1 MGENQALARLESLLRPR.....KEAAEFLGFSYAPPTDSFL 445

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2150	91.9	431	4	US-09-031-295-2
2	2146	91.7	431	2	US-08-712-709-5
3	2146	91.7	431	3	US-09-111-444-5
4	2146	91.7	431	4	US-09-541-228-5
5	2100.5	89.8	430	2	US-08-712-709-9
6	2100.5	89.8	430	3	US-09-111-444-9
7	2100.5	89.8	430	4	US-09-541-228-9
8	861	36.8	480	3	US-09-091-058-2
9	810.5	34.6	482	4	US-09-430-564-2
10	810.5	34.6	495	4	US-09-430-564-3
11	807	34.5	525	2	US-08-749-902-7
12	807	34.5	525	2	US-08-749-902-8
13	807	34.5	525	4	US-09-430-564-16
14	775	33.1	671	6	5266464-2
15	774.5	33.1	587	1	US-08-313-274-2
16	696.5	29.8	350	4	US-09-457-040B-37
17	696.5	29.8	351	4	US-09-457-040B-6
18	695	29.7	1151	4	US-09-457-040B-11
19	694.5	29.7	676	4	US-09-313-930-2
20	669.5	28.6	264	2	US-07-857-224B-15
21	666.5	28.5	264	2	US-07-857-224B-10
22	666	28.5	268	4	US-09-430-564-12
23	665.5	28.4	264	2	US-07-857-224B-12
24	661.5	28.3	263	2	US-07-857-224B-13
25	661.5	28.3	264	2	US-07-857-224B-17
26	658	28.1	269	2	US-07-857-224B-14
27	657.5	28.1	264	2	US-07-857-224B-11

28	654	27.9	269	2	US-07-857-224B-16	Sequence 16, Appl
29	649.5	27.8	258	4	US-09-430-564-6	Sequence 6, Appl
30	636.5	27.2	260	2	US-07-857-224B-4	Sequence 4, Appl
31	632.5	27.0	260	2	US-07-857-224B-3	Sequence 3, Appl
32	624.5	26.7	260	2	US-07-857-224B-2	Sequence 2, Appl
33	620.5	26.5	260	2	US-07-857-224B-8	Sequence 8, Appl
34	618.5	26.4	260	2	US-07-857-224B-1	Sequence 1, Appl
35	612.5	26.2	260	2	US-08-061-636-4	Sequence 4, Appl
36	612.5	26.2	260	2	US-07-857-224B-6	Sequence 6, Appl
37	612.5	26.2	260	5	PCT-US94-05268-4	Sequence 4, Appl
38	610.5	26.1	260	2	US-07-857-224B-7	Sequence 7, Appl
39	608.5	26.0	272	3	US-08-908-332-8	Sequence 8, Appl
40	561	24.0	556	2	US-09-016-000-4	Sequence 4, Appl
41	559	23.9	900	2	US-08-630-822A-62	Sequence 62, Appl
42	559	23.9	900	2	US-09-005-069-62	Sequence 62, Appl
43	559	23.9	900	4	US-09-171-156A-21	Sequence 21, Appl
44	557.5	23.8	258	2	US-07-857-224B-5	Sequence 5, Appl
45	549	23.5	416	4	US-09-457-040B-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-031-295-2
; Sequence 2, Application US/09031295
; Patent No. 6326181
; GENERAL INFORMATION:
; APPLICANT: LANG, Florian
; APPLICANT: WALDEGGER, Tubingen
; TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/031,295
; FILING DATE: 26-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 197-08-173.8
; FILING DATE: 28-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 058315/0123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 431 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-031-295-2

Query Match 91.9%; Score 2150; DB 4; Length 431;
Best Local Similarity 99.5%; Pred. No. 1.1e-194;
Matches 405; Conservative 0; Indels 0; Gaps 0;
Qy 39 LAFMKQRRMGLNFIQKIANNYSACKHPEVQSILKISQPELMNANPPSPSQIN 98
Db 25 IAFMKQRRMGLNFIQKIANNYSACKHPEVQSILKISQPELMNANPPSPSQIN 84

QY 99 LGPSSNPHAKPSDFHFLKVIKSGFGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 158
DB 85 LGPSSNPHAKPSDFHFLKVIKSGFGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 144
QY 159 SERNVLLKNVKHPPFLVGLHFSFQADKLYFVLDYINGGELFYHLQRCERCFLEPRARFYAA 218
DB 145 SERNVLLKNVKHPPFLVGLHFSFQADKLYFVLDYINGGELFYHLQRCERCFLEPRARFYAA 204
QY 219 EIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTDGFLCKENIEHNSSTTSTFCGTPEYL 278
DB 205 EIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTDGFLCKENIEHNSSTTSTFCGTPEYL 264
QY 279 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNIILNKPLQLKPNITNSA 338
DB 265 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNIILNKPLQLKPNITNSA 324
QY 339 RHLLEGLLQKDRTRKLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFNPVNSGPNDLRH 398
DB 325 RHLLEGLLQKDRTRKLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFNPVNSGPNELRH 384
QY 399 FDPFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 445
DB 385 FDPFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 431

RESULT 2

US-08-712-709-5
; Sequence 5, Application US/08712709
; Patent No. 5863780

; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA

; COUNTRY: U.S.
; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08712,709

; FILING DATE: Filed Herewith

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0118 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 431 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; IMMEDIATE SOURCE:

; LIBRARY:

; CLONE: Consensus

US-08-712-709-5

Query Match 91.7%; Score 2146; DB 2; Length 431;
Best Local Similarity 99.5%; Pred. No. 2.6e-194;
Matches 405; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 39 LAFMKORRMGLNDFIOKIANNSSVACHPEVQSILKISQOEPELMNANSPPPSPSQOIN 98
DB 25 LAFMKORRMGLNDFIOKIANNSSVACHPEVQSILKISQOEPELMNANSPPPSPSQOIN 84
QY 99 LGPSSNPHAKPSDFHFLKVIKSGFGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 158
DB 85 LGPSSNPHAKPSDFHFLKVIKSGFGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 144
QY 159 SERNVLLKNVKHPPFLVGLHFSFQADKLYFVLDYINGGELFYHLQRCERCFLEPRARFYAA 218
DB 145 SERNVLLKNVKHPPFLVGLHFSFQADKLYFVLDYINGGELFYHLQRCERCFLEPRARFYAA 204
QY 219 EIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTDGFLCKENIEHNSSTTSTFCGTPEYL 278
DB 205 EIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTDGFLCKENIEHNSSTTSTFCGTPEYL 264
QY 279 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNIILNKPLQLKPNITNSA 338
DB 265 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNIILNKPLQLKPNITNSA 324
QY 339 RHLLEGLLQKDRTRKLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFNPVNSGPNDLRH 398
DB 325 RHLLEGLLQKDRTRKLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFNPVNSGPNDLRH 384
QY 399 FDPFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 445
DB 385 FDPFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 431

RESULT 3

US-09-111-444-5

; Sequence 5, Application US/09111444

; Patent No. 6045792

; GENERAL INFORMATION:

; APPLICANT: Au-Young, Janice

; APPLICANT: Guegler, Karl J.

; APPLICANT: Hawkins, Phillip R.

; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/111,444

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/712,709

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0118 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 431 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; IMMEDIATE SOURCE:

LIBRARY: Consensus
US-09-541-444-5

Query Match 91.7%; Score 2146; DB 3; Length 431;
Best Local Similarity 99.5%; Pred. No. 2.6e-194;
Matches 405; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 39 LAFWKQRRMGLNDFIQKIANNYSACKHPEVQSILKISQOPEPELMNANPPSPSPSQOIN 98
DB 25 IAFWKQRRMGLNDFIQKIANNYSACKHPEVQSILKISQOPEPELMNANPPSPSPSQOIN 84

QY 99 LQSSNPFAKPSDFHFLKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 159
DB 85 LQSSNPFAKPSDFHFLKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 144

QY 159 SERNVLLKNVKGHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRCERCFLEPRARYAA 218
DB 145 SERNVLLKNVKGHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRCERCFLEPRARYAA 204

QY 219 EIASALGYLHSLNIVYRDLPENILDSQGHIVLTDGCLCKENIEHNSTTSTFCGTPEYL 278
DB 205 EIASALGYLHSLNIVYRDLPENILDSQGHIVLTDGCLCKENIEHNSTTSTFCGTPEYL 264

QY 279 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLQKENITNSA 338
DB 265 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLQKENITNSA 324

QY 339 RHLLEGLLQKDRTRKLGAKDDFMEIKSHVFFSLINWDDLINNKITPPFPNPNVSGPNDLRH 398
DB 325 RHLLEGLLQKDRTRKLGAKDDFMEIKSHVFFSLINWDDLINNKITPPFPNPNVSGPNDLRH 384

QY 399 FDPFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 445
DB 385 FDPFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 431

RESULT 4

US-09-541-228-5
Sequence 5, Application US/09541228
Patent No. 6232077
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/541.228
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/712,709
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4186
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 431 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY:

CLONE: Consensus

US-09-541-228-5

Query Match 91.7%; Score 2146; DB 4; Length 431;
Best Local Similarity 99.5%; Pred. No. 2.6e-194;
Matches 405; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 39 LAFWKQRRMGLNDFIQKIANNYSACKHPEVQSILKISQOPEPELMNANPPSPSPSQOIN 98
DB 25 IAFWKQRRMGLNDFIQKIANNYSACKHPEVQSILKISQOPEPELMNANPPSPSPSQOIN 84

QY 99 LQSSNPFAKPSDFHFLKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 158
DB 85 LQSSNPFAKPSDFHFLKVIKGSFGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 144

QY 159 SERNVLLKNVKGHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRCERCFLEPRARYAA 218
DB 145 SERNVLLKNVKGHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRCERCFLEPRARYAA 204

QY 219 EIASALGYLHSLNIVYRDLPENILDSQGHIVLTDGCLCKENIEHNSTTSTFCGTPEYL 278
DB 205 EIASALGYLHSLNIVYRDLPENILDSQGHIVLTDGCLCKENIEHNSTTSTFCGTPEYL 264

QY 279 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLQKENITNSA 338
DB 265 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLQKENITNSA 324

QY 339 RHLLEGLLQKDRTRKLGAKDDFMEIKSHVFFSLINWDDLINNKITPPFPNPNVSGPNDLRH 398
DB 325 RHLLEGLLQKDRTRKLGAKDDFMEIKSHVFFSLINWDDLINNKITPPFPNPNVSGPNDLRH 384

QY 399 FDPFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 445
DB 385 FDPFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 431

RESULT 5

US-08-712-709-9
Sequence 9, Application US/08712709
Patent No. 5863780
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,709
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 294637
US-08-712-709-9

Query Match 89.8%; Score 2100.5; DB 2; Length 430;
Best Local Similarity 97.1%; Pred. No. 5.1e-190;
Matches 395; Conservative 7; Mismatches 4; Indels 1; Gaps 1;
QY 39 LAFMKQRRMGNDFIQKIANNYSACKHPEVOSILKISQPOPELMNANSPSPSPSOQIN 98
DB 25 IAFMKQRRMGNDFIQKIANNYSACKHPEVOSYLYKISQPOPELMNANSPSPSPSOQIN 84
QY 99 LQSSNPHAKPSDFHFLKVIKIGSGFGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 158
DB 85 LQSSNPHAKPSDFHFLKVIKIGSGFGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 144
QY 159 SERNVLLKNVHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRCFCLEPRARFYAA 218
DB 145 SERNVLLKNVHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRCFCLEPRARFYAA 204
QY 219 EIASALGYLHSLNIVYRDLPENILDSQGHIVLTDGLCKENIEHNSTTSTFCGTPEYL 278
DB 205 EIASALGYLHSLNIVYRDLPENILDSQGHIVLTDGLCKENIEHNSTTSTFCGTPEYL 264
QY 279 APEVLHKQPYDRTVDWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLQK-NITNSA 338
DB 265 APEVLHKQPYDRTVDWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLQK-NITNSA 323
QY 339 RHLLEGLLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLINNKITPPFPNPNVSGPDLRH 398
DB 324 RHLLEGLLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLINNKITPPFPNPNVSGPDLRH 383
QY 399 FDPEFTEEPVNSIGKSPDSVLVTASVKEAAEFLGFSYAPPTDSFL 445
DB 384 FDPEFTEEPVNSIGKSPDSVLVTASVKEAAEFLGFSYAPPTDSFL 430

RESULT 6
US-09-111-444-9
Sequence 9, Application US/09111444
Patent No. 6045792
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/111.444
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/712,709
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 294637
US-09-111-444-9
Query Match 89.8%; Score 2100.5; DB 3; Length 430;
Best Local Similarity 97.1%; Pred. No. 5.1e-190;
Matches 395; Conservative 7; Mismatches 4; Indels 1; Gaps 1;
QY 39 LAFMKQRRMGNDFIQKIANNYSACKHPEVOSILKISQPOPELMNANSPSPSPSOQIN 98
DB 25 IAFMKQRRMGNDFIQKIANNYSACKHPEVOSYLYKISQPOPELMNANSPSPSPSOQIN 84
QY 99 LQSSNPHAKPSDFHFLKVIKIGSGFGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 158
DB 85 LQSSNPHAKPSDFHFLKVIKIGSGFGKVLARHKAEEVFYAVKVLQKAILKKKEEKHIM 144
QY 159 SERNVLLKNVHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRCFCLEPRARFYAA 218
DB 145 SERNVLLKNVHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRCFCLEPRARFYAA 204
QY 219 EIASALGYLHSLNIVYRDLPENILDSQGHIVLTDGLCKENIEHNSTTSTFCGTPEYL 278
DB 205 EIASALGYLHSLNIVYRDLPENILDSQGHIVLTDGLCKENIEHNSTTSTFCGTPEYL 264
QY 279 APEVLHKQPYDRTVDWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLQK-NITNSA 338
DB 265 APEVLHKQPYDRTVDWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLQK-NITNSA 323
QY 339 RHLLEGLLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLINNKITPPFPNPNVSGPDLRH 398
DB 324 RHLLEGLLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLINNKITPPFPNPNVSGPDLRH 383
QY 399 FDPEFTEEPVNSIGKSPDSVLVTASVKEAAEFLGFSYAPPTDSFL 445
DB 384 FDPEFTEEPVNSIGKSPDSVLVTASVKEAAEFLGFSYAPPTDSFL 430

RESULT 7
US-09-541-228-9
Sequence 9, Application US/09541228
Patent No. 6232077
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:

Best Local Similarity 44.6%; Pred. No. 3.4e-68;
Matches 173; Conservative 65; Mismatches 111; Indels 39; Gaps 12;
Qy 79 EPELMANPSP-----PPSPSQ-----INLGPSS-NPHAKPSDFHFLKVIGK 120
Db 20 EPELSPADACPLAELRAAGLEPVGHYEVELTETSVNNGPERIGPHC-----FELLRLVIGK 75
Qy 121 GSGFKVLLARHKAEEV----FYAVKVLQKAILKK-KEEKHIMSERVLLKNVKKHPLVG 175
Db 76 GYGKVFQVR-KVOGTNLGKIYAMKVLKAKI VRNAKDTAHTRAERNI-LESVKHGFIVE 133
Qy 176 LHFSFOTADKLYFVLDYINGGELFYHLQRECFLEPRARYAAEIASALGYLHSLNIYVR 235
Db 134 LAYAFQTGGKLYLLECLSGGELFTHLEREGIFLEDACFYLAETILALGHLSQGIYR 193
Qy 236 DLKPENILSSQGHIVLTDGLCKENIEHNSSTSTFCGTPEYLAPEVLHKQPYDRTVDWW 295
Db 194 DLKPENILSSQGHIVLTDGLCKESIHGAVTHTCGTIEYMAPEILVRSGHNRADWW 253
Qy 296 CLGAVLYEMLYGLPPFYSRNTAEMYNILNKPLQKNTNSARHLLGLOKDRTKRL- 354
Db 254 SLGALMYDMITGSPPTAENRRKTKMDKIIRGKLALPPYLTDPDARDLVKKFLKRNPSORIG 313
Qy 355 GAKDDFMEIKSHVFFSLINDDLINKKITPPFPNPNVSGPNDLRFHDFDEFTEE-PVPNSIG 413
Db 314 GPGDADVQVRHPPFRHNMWDDLLAWRDPFPCQSEEDVSQFDRTRFTQTPV----- 368
Qy 414 KSPDSVLVTASVKEAAEAFGFSYAPPT 441
Db 369 DSPDD---TALSANQAFLGFTYVAPS 393

RESULT 10
US-09-430-564-3
; Sequence 3, Application US/09430564
; Patent No. 6372467
; GENERAL INFORMATION:
; APPLICANT: John Blenis
; APPLICANT: Kay K. Lee-Fruman
; APPLICANT: Calvin J. Kuo
; TITLE OF INVENTION: P54S6K AND P85S6K GENES, PROTEINS,
; FILE REFERENCE: 00246/506002
; CURRENT APPLICATION NUMBER: US/09/430,564
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/106,141
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-564-3

Query Match 34.6%; Score 810.5; DB 4; Length 495;
Best Local Similarity 44.6%; Pred. No. 3.6e-68;
Matches 173; Conservative 65; Mismatches 111; Indels 39; Gaps 12;
Qy 79 EPELMANPSP-----PPSPSQ-----INLGPSS-NPHAKPSDFHFLKVIGK 120
Db 33 EPELSPADACPLAELRAAGLEPVGHYEVELTETSVNNGPERIGPHC-----FELLRLVIGK 88
Qy 121 GSGFKVLLARHKAEEV----FYAVKVLQKAILKK-KEEKHIMSERVLLKNVKKHPLVG 175
Db 89 GYGKVFQVR-KVOGTNLGKIYAMKVLKAKI VRNAKDTAHTRAERNI-LESVKHGFIVE 146
Qy 176 LHFSFOTADKLYFVLDYINGGELFYHLQRECFLEPRARYAAEIASALGYLHSLNIYVR 235
Db 147 LAYAFQTGGKLYLLECLSGGELFTHLEREGIFLEDACFYLAETILALGHLSQGIYR 206
Qy 236 DLKPENILSSQGHIVLTDGLCKENIEHNSSTSTFCGTPEYLAPEVLHKQPYDRTVDWW 295

Db 207 DLKPENILSSQGHIVLTDGLCKESIHGAVTHTCGTIEYMAPEILVRSGHNRADWW 266
Qy 296 CLGAVLYEMLYGLPPFYSRNTAEMYNILNKPLQKNTNSARHLLGLOKDRTKRL- 354
Db 267 SLGALMYDMITGSPPTAENRRKTKMDKIIRGKLALPPYLTDPDARDLVKKFLKRNPSORIG 326
Qy 355 GAKDDFMEIKSHVFFSLINDDLINKKITPPFPNPNVSGPNDLRFHDFDEFTEE-PVPNSIG 413
Db 327 GPGDADVQVRHPPFRHNMWDDLLAWRDPFPCQSEEDVSQFDRTRFTQTPV----- 381
Qy 414 KSPDSVLVTASVKEAAEAFGFSYAPPT 441
Db 382 DSPDD---TALSANQAFLGFTYVAPS 406

RESULT 11
US-08-749-902-7
; Sequence 7, Application US/08749902
; Patent No. 5985635
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
; TITLE OF INVENTION: PROTEIN KINASES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA: US/08/749,902
; APPLICATION NUMBER: US/08/749,902
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0150 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 525 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 189508
US-08-749-902-7

Query Match 34.5%; Score 807; DB 2; Length 525;
Best Local Similarity 46.8%; Pred. No. 8.3e-68;
Matches 164; Conservative 63; Mismatches 105; Indels 20; Gaps 9;
Qy 97 INLGPSSNPHAKPSDFHFLKVIGKSGFGKVLARH-----KAEVVFVAVKVLQKAILKK- 151
Db 79 VNGPEK---IRPECELLEVLVGKGVKVFQVRYKVTGANTGKIF-AMKVLKKAIVRNA 134
Qy 152 KEEKHIMSERVLLKNVKKHPLVGLHFSFOTADKLYFVLDYINGGELFYHLQRECFLEP 211
Db 135 KDTAHTKAERNI-LEEVGHPFIVLDIYAFQTGKLYLLELVLGGELFMQREGIFMED 193

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2003, 19:14:32 ; Search time 73 Seconds
(without alignments)
812.281 Million cell updates/sec

Title: US-10-067-977-2
Perfect score: 2340
Sequence: 1 MGEWQALARLESLLRR.....KEAAEAFLGFSYAPPTDSFL 445

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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 - 22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
 - 23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2154	92.1	431	20	AAW90139 Human sgk protein.
2	2150	91.9	431	19	AAW77217 Human cell-volme
3	2150	91.9	431	21	AAW24115 Human serum and gl
4	2150	91.9	431	22	AAW65613 Novel protein kina
5	2146	91.7	431	19	AAW54025 Human protein kina
6	2141	91.5	431	21	AAW95279 Human serum and gl
7	2118	90.5	431	21	AAW24116 Rat serum and gluc
8	2118	90.5	431	21	AAW93550 A rat serum and gl
9	2052.5	87.7	430	22	AAW65614 Novel protein kina
10	1992	85.1	388	20	AAW48573 Human breast tumou

11	1976	84.4	373	22	AAW99815	AGC protein kinase
12	1699	72.6	321	22	AAW99836	AGC protein kinase
13	1481	63.3	496	20	AAW87772	Human serum glucoc
14	1476	63.1	429	21	AAW95378	Human serum and gl
15	1476	63.1	496	22	AAW87228	Novel central nerv
16	1476	63.1	496	22	AAW87382	Novel central nerv
17	1476	63.1	496	22	AAW40820	Human polypeptide
18	1463	62.5	429	21	AAW24114	Human serine threo
19	1461	62.4	496	22	AAW38834	Human polypeptide
20	1419	60.6	427	21	AAW95376	Human serum and gl
21	1413.5	60.4	382	22	AAW25594	Human protein sequ
22	1411	60.3	367	21	AAW95375	Human serum and gl
23	1411	60.3	367	22	AAW28087	Novel human secret
24	1411	60.3	367	23	AAW22765	Novel human secret
25	1409	60.2	367	22	AAW65708	Novel protein kina
26	1387	59.3	367	21	AAW95377	Mouse serum and gl
27	1281	54.7	464	22	AAW93732	Human polypeptide
28	1267.5	54.2	319	22	AAW99838	AGC protein kinase
29	1254.5	53.6	322	22	AAW99837	AGC protein kinase
30	1227	52.4	446	22	AAW65616	Novel protein kina
31	968.5	41.4	276	22	AAW87658	Novel central nerv
32	968.5	41.4	276	22	AAU17104	Novel signal trans
33	955.5	40.8	244	22	AAW65615	Novel protein kina
34	916	39.1	479	21	AAW19284	Amino acid sequenc
35	916	39.1	479	21	AAW13393	Human Akt-3. Homo
36	916	39.1	479	23	AAW79420	Human protein kina
37	916	39.1	479	23	ABW06998	Human Akt3 protein
38	912	39.0	465	21	AAW19011	Amino acid sequenc
39	912	39.0	465	22	AAW78018	Human Akt3. Homo
40	912	39.0	465	22	AAW19996	Human serine/threo
41	912	39.0	465	22	AAW19998	Human serine/threo
42	910	38.9	454	22	AAW78021	Akt3 related polyp
43	908	38.8	479	21	AAW43132	Human ORFX ORF2896
44	894	38.2	530	22	ABW66370	Drosophila melanog
45	894	38.2	530	22	ABW71272	Drosophila melanog

ALIGNMENTS

RESULT 1																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				</
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DR N-PSDB; AAV74190.
XX
PT Treating chronic renal failure, diabetic nephropathy and Alzheimer's
PT disease - by administration of nucleic acids and antagonists which
PT inhibit activity or expression of human serum glucocorticoid
PT regulated kinase (sgk), a serine/threonine protein kinase
XX
XX
PS Disclosure; Page 16-17; 17pp; English.
XX
CC This sequence represents a novel human serum glucocorticoid regulated
CC kinase (sgk) protein which is a member of the serine/threonine protein
CC kinase family. This protein is used for the treatment of a subject having
CC need to inhibit/antagonise activity or expression of human sgk
CC polypeptide e.g. for the treatment of chronic renal failure, diabetic
CC nephropathy, inflammation, Alzheimer's disease and wounds.
XX
SQ Sequence 431 AA;
Query Match 92.1%; Score 2154; DB 20; Length 431;
Best Local Similarity 99.8%; Pred. No. 2.9e-192;
Matches 406; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 39 LAFMKQRRMGLNDFIQKIANNYSACKHPEVQSILKISQOPELMNANPPSPSQOIN 98
DB 25 IAFMKQRRMGLNDFIQKIANNYSACKHPEVQSILKISQOPELMNANPPSPSQOIN 84
QY 99 LGSNNPHAKPSDFHFLKVGSGFGKVLARHKAEEVFYAVKLOKAILKKKEKHIM 158
DB 85 LGSNNPHAKPSDFHFLKVGSGFGKVLARHKAEEVFYAVKLOKAILKKKEKHIM 144
QY 159 SERVLKQVDPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPQLKPNITNSA 218
DB 145 SERVLKQVDPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPQLKPNITNSA 204
QY 219 EIASALGYLHSLNIVYRDLKPNILDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 278
DB 205 EIASALGYLHSLNIVYRDLKPNILDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 264
QY 279 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPQLKPNITNSA 338
DB 325 RHLLEGLQKDRTKRLGAKDDFMEIKSHVFFSLINWDDLINCKITPPFPNVSGPNDLRH 384
QY 399 FDPFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 445
DB 385 FDPFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 431
RESULT 2
AAW77217
ID AAW77217 standard; Protein; 431 AA.
AC AAW77217;
XX
XX 16-NOV-1998 (first entry)
DT
XX Human cell-volume regulating kinase h-sgk.
DE
XX Human; cell-volume; kinase; h-sgk; diabetes mellitus;
KW renal insufficiency; inflammation; Alzheimer's disease.
XX
OS Homo sapiens.
XX
XX EP861896-A2.
XX
XX 02-SEP-1998.
PD
XX 27-JAN-1998; 98EP-0101338.
PF
XX 28-FEB-1997; 97DE-1008173.
PR

XX
PA (DADE-) DADE BEHRING MARBURG GMBH.
XX
PI Lang F, Waldegger S;
XX
XX WPI; 1998-449109/39.
DR
DR N-PSDB; AAV48311.
XX
XX New nucleic acid encoding cell-volume regulating kinase h-sgk and
PT related proteins - used for diagnosis and treatment of diseases
PT involving changes in cell volume, e.g. renal insufficiency,
PT inflammation, infections etc.
XX
XX Disclosure; Fig 1; 15pp; German.
PS
XX The human cell-volume regulating kinase h-sgk is inhibited by the
CC swelling of cells (or presence of urea), whereas cell shrinkage
CC stimulates its expression. The nucleic acid h-sgk, and fragments, are
CC particularly used to detect changes in cell volume, specifically for
CC diagnosis of conditions that involve such changes, e.g. hyper- and hypo-
CC natriemia, diabetes mellitus, renal insufficiency, hypercatabolism,
CC hepatic encephalopathy, inflammation, microbial/viral infection, fructose
CC intolerance, hyper- and hypo-glycaemia and Alzheimer's disease.
CC The nucleic acid, protein and products including receptors that bind
CC h-sgk, can be used to treat these disorders.
XX
SQ Sequence 431 AA;
Query Match 91.9%; Score 2150; DB 19; Length 431;
Best Local Similarity 99.5%; Pred. No. 6.8e-192;
Matches 405; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 39 LAFMKQRRMGLNDFIQKIANNYSACKHPEVQSILKISQOPELMNANPPSPSQOIN 98
DB 25 IAFMKQRRMGLNDFIQKIANNYSACKHPEVQSILKISQOPELMNANPPSPSQOIN 84
QY 99 LGSNNPHAKPSDFHFLKVGSGFGKVLARHKAEEVFYAVKLOKAILKKKEKHIM 158
DB 85 LGSNNPHAKPSDFHFLKVGSGFGKVLARHKAEEVFYAVKLOKAILKKKEKHIM 144
QY 159 SERVLKQVDPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPQLKPNITNSA 218
DB 145 SERVLKQVDPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPQLKPNITNSA 204
QY 219 EIASALGYLHSLNIVYRDLKPNILDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 278
DB 205 EIASALGYLHSLNIVYRDLKPNILDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 264
QY 279 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPQLKPNITNSA 338
DB 265 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPQLKPNITNSA 324
QY 339 RHLLEGLQKDRTKRLGAKDDFMEIKSHVFFSLINWDDLINCKITPPFPNVSGPNDLRH 398
DB 325 RHLLEGLQKDRTKRLGAKDDFMEIKSHVFFSLINWDDLINCKITPPFPNVSGPNDLRH 384
QY 399 FDPFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 445
DB 385 FDPFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 431
RESULT 3
AAB24115
ID AAB24115 standard; Protein; 431 AA.
AC AAB24115;
XX
XX 29-JAN-2001 (first entry)
DT
XX Human serum and glucocorticoid regulated kinase protein (HSGK).
DE
XX Human; STK3; serine threonine kinase; HSGK; RSGK;
KW serum and glucocorticoid regulated kinase.
KW

XX OS Homo sapiens.
 XX CN1259573-A.
 XX 12-JUL-2000.
 XX 29-OCT-1998; 98CN-0123822.
 XX 29-OCT-1998; 98CN-0123822.
 XX (UYFU-) UNIV FUDAN.
 XX Yu L, Fu Q, Zhao Y;
 XX WPI; 2000-587991/56.
 XX New human serine threonine protein kinase, its code sequence,
 XX preparation, and use -
 XX Example 3; Fig 3; 29pp; Chinese.
 XX The present invention describes human serine threonine kinase STK3,
 XX which is a new member of the serine/threonine protein kinase family.
 XX Human STK3 shares homology with human serum and glucocorticoid
 XX regulated kinase (HSGK) and rat SGK (RSGK). The present sequence
 XX represents the human HSGK protein sequence from the present invention.
 XX SQ Sequence 431 AA;
 Query Match 91.9%; Score 2150; DB 21; Length 431;
 Best Local Similarity 99.5%; Pred. No. 6.8e-192;
 Matches 405; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 39 LAFMKQRRMGLNDFIQKIANNNSYACKHPEVQSILKISQPOPELMNANPPSPSQOIN 98
 DB 25 IAFMKQRRMGLNDFIQKIANNNSYACKHPEVQSILKISQPOPELMNANPPSPSQOIN 84
 QY 99 LGPSSNPHAKPSDFHFLKVGKSGFGKVLARHKAEEVFYAVKLOKAILKKKEKHIM 158
 DB 85 LGPSSNPHAKPSDFHFLKVGKSGFGKVLARHKAEEVFYAVKLOKAILKKKEKHIM 144
 QY 159 SERVLKKNVKHPLVGLHFSFQTADKLYFVLVDYINGGELFYHLQERCFLEPRARYAA 218
 DB 145 SERVLKKNVKHPLVGLHFSFQTADKLYFVLVDYINGGELFYHLQERCFLEPRARYAA 204
 QY 219 EIASALGYLHSLNIVYRDLKPNILLDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 278
 DB 205 EIASALGYLHSLNIVYRDLKPNILLDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 264
 QY 279 APEVLHKQPYDRTVDWVWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLKPNITNSA 338
 DB 265 APEVLHKQPYDRTVDWVWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLKPNITNSA 324
 QY 339 RHLLEGLLQDKRTKRLGAKDPMFEEKSHVFFSLINWDDLKIKITPPFNPNVSGPNDLRH 398
 DB 325 RHLLEGLLQDKRTKRLGAKDPMFEEKSHVFFSLINWDDLKIKITPPFNPNVSGPNELRH 384
 QY 399 FDFEFTPEPNSIGKSPDSVLVTASVKEAAEAPLGFSYAPPTDSFL 445
 DB 385 FDFEFTPEPNSIGKSPDSVLVTASVKEAAEAPLGFSYAPPTDSFL 431
 RESULT 4
 AAB65613
 ID AAB65613 standard; Protein; 431 AA.
 XX AC AAB65613;
 XX 27-MAR-2001 (first entry)
 XX Novel protein kinase, SEQ ID NO: 139.
 XX

KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
 KW immunosuppressive; cardiant; renal; antiinflammatory; antiaesthetic;
 KW dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;
 KW immune disorder; cardiovascular disease; neurodegenerative disease;
 KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
 KW inflammatory pelvic disease; multiple sclerosis; psoriasis.
 XX Homo sapiens.
 XX WO200073469-A2.
 XX 07-DEC-2000.
 XX 26-MAY-2000; 2000WO-US14842.
 XX 28-MAY-1999; 99US-0136503.
 XX (SUGB-) SUGEN INC.
 XX PLOWMAN GD, Martinez R, Whyte D, Sudersanam S;
 XX WPI; 2001-032161/04.
 XX N-PSDB; AAF44639.
 XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
 XX treating immune-related diseases and disorders, cardiovascular disease,
 XX neurodegenerative diseases and/or cancers -
 XX Claim 10; Fig 1; 310pp; English.
 XX The present sequence is a novel protein kinase. The novel protein kinases
 XX and the nucleic acids that encode them may be used in the treatment and
 XX diagnosis of diseases associated with inappropriate kinase expression
 XX such as immune-related diseases and disorders, cardiovascular disease,
 XX neurodegenerative diseases and/or cancers. The nucleic acids and
 XX complementary sequences may also be used as DNA probes in diagnostic
 XX assays. The kinase polypeptides may be used as antigens in the production
 XX of antibodies of kinase expression and activity. Anti-kinase antibodies
 XX and kinase antagonists may also be used to down regulate kinase
 XX expression and activity. Diseases related to kinase expression and
 XX activity include rheumatoid arthritis, atherosclerosis, autoimmune
 XX disorders, complications of organ transplantation, myocardial infarction,
 XX immune disorders, cardiomyopathies, strokes, renal failure,
 XX oxidative-stress related disorders, chronic inflammatory bowel disease,
 XX chronic inflammatory pelvic disease, multiple sclerosis, asthma,
 XX osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and
 XX reproductive disorders.
 XX SQ Sequence 431 AA;
 Query Match 91.9%; Score 2150; DB 22; Length 431;
 Best Local Similarity 99.5%; Pred. No. 6.8e-192;
 Matches 405; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 39 LAFMKQRRMGLNDFIQKIANNNSYACKHPEVQSILKISQPOPELMNANPPSPSQOIN 98
 DB 25 IAFMKQRRMGLNDFIQKIANNNSYACKHPEVQSILKISQPOPELMNANPPSPSQOIN 84
 QY 99 LGPSSNPHAKPSDFHFLKVGKSGFGKVLARHKAEEVFYAVKLOKAILKKKEKHIM 158
 DB 85 LGPSSNPHAKPSDFHFLKVGKSGFGKVLARHKAEEVFYAVKLOKAILKKKEKHIM 144
 QY 159 SERVLKKNVKHPLVGLHFSFQTADKLYFVLVDYINGGELFYHLQERCFLEPRARYAA 218
 DB 145 SERVLKKNVKHPLVGLHFSFQTADKLYFVLVDYINGGELFYHLQERCFLEPRARYAA 204
 QY 219 EIASALGYLHSLNIVYRDLKPNILLDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 278
 DB 205 EIASALGYLHSLNIVYRDLKPNILLDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 264
 QY 279 APEVLHKQPYDRTVDWVWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLKPNITNSA 338
 DB 265 APEVLHKQPYDRTVDWVWCLGAVLYEMLYGLPPFYSRNTAEYDNLNKPQLKPNITNSA 324

QY 339 RHLLEGLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLKINKITPPFPNVSGPNDLRH 398
 DB 325 RHLLEGLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLKINKITPPFPNVSGPNDLRH 384
 QY 399 FDPEFTTEEPVNSIGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 445
 DB 385 FDPEFTTEEPVNSIGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 431

RESULT 5

AAW54025
 ID AAW54025 standard; Protein; 431 AA.

XX AC AAW54025;

XX DT 31-JUL-1998 (first entry)

XX DE Human protein kinase HPK-3.

XX OS Homo sapiens.

XX PN WO9811234-A2.

XX PD 19-MAR-1998.

XX PF 10-SEP-1997; 97WO-US15923.

XX PR 12-SEP-1996; 96US-0712709.

XX PA (INCY-) INCYTE PHARM INC.

XX PI Au-Young J, Guegler KJ, Hawkins PR;

XX DR WPI; 1998-207394/18.

XX DR N-PSDB; AAV23833.

XX PT New isolated human protein kinase(s) - used to develop products for

XX PT diagnosis and treatment of e.g. Alzheimer's disease, cancers,

XX PT asthma, multiple sclerosis or rheumatoid arthritis

XX PS Claim 23; Fig 3; 75pp; English.

XX CC This sequence is a human protein kinase (HPK) of the invention. The

XX CC HPK protein can be used to develop products for studying signalling

XX CC cascades in various cells and tissues, diagnosing disease and selecting

XX CC inhibitors or drugs with the potential to intervene in various disorders

XX CC or diseases in which altered kinase expression is implicated. The

XX CC products can be used to e.g. reverse memory loss such as due to

XX CC Alzheimer's disease, for cancer treatment or to provide anti-inflammatory

XX CC and immunosuppressive effects in the treatment of e.g. asthma, multiple

XX CC sclerosis, rheumatoid arthritis, as well as certain cancers, e.g.

XX CC lymphocytic leukaemias or lymphomas.

XX SQ Sequence 431 AA;

Query Match 91.7%; Score 2146; DB 19; Length 431;

Best Local Similarity 99.5%; Pred. No. 1.6e-191;

Matches 405; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 39 LAFMKQRMGLNDFIQIANNYSACKHPEVQSILKISQOPELWNNANPPSPSQOIN 98

DB 25 IAFMKQRMGLNDFIQIANNYSACKHPEVQSILKISQOPELWNNANPPSPSQOIN 84

QY 99 LGPSSNPHAKPSDFHFLKVIKSGFGKVLARHKAEEVFVAVKVLQKAILKKKEKHIM 158

DB 85 LGPSSNPHAKPSDFHFLKVIKSGFGKVLARHKAEEVFVAVKVLQKAILKKKEKHIM 144

QY 159 SERNVLLKNVKKHFFLVGLHFSQTADKLYFVLVDYINGGELFYHLQERCFLEPRARYAA 218
 DB 145 SERNVLLKNVKKHFFLVGLHFSQTADKLYFVLVDYINGGELFYHLQERCFLEPRARYAA 204
 QY 219 ETASALGYLHSLNIVYRDILKPNENILDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 278
 DB 205 ETASALGYLHSLNIVYRDILKPNENILDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 264
 QY 279 APEVLHKQPYDRTDVMWCLGAVLYEMLYGLPPFYSRNTAEMVDNIINKPLQKLPNITNSA 338
 DB 265 APEVLHKQPYDRTDVMWCLGAVLYEMLYGLPPFYSRNTAEMVDNIINKPLQKLPNITNSA 324
 QY 339 RHLLEGLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLKINKITPPFPNVSGPNDLRH 398
 DB 325 RHLLEGLQKQRTKRLGAKDDFMEIKSHVFFSLINWDDLKINKITPPFPNVSGPNDLRH 384
 QY 399 FDPEFTTEEPVNSIGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 445
 DB 385 FDPEFTTEEPVNSIGKSPDSVLVTASVKEAAEAFGLFSYAPPTDSFL 431

RESULT 6

AAV95279
 ID AAV95279 standard; Protein; 431 AA.

XX AC AAV95279;

XX DT 12-SEP-2000 (first entry)

XX DE Human serum and glucocorticoid-induced protein kinase.

XX KW Serum and glucocorticoid-induced protein kinase; SGK;

XX KW human; phosphorylation; cancer; diabetes; ischaemia; therapy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Modified-site 256

XX FT Modified-site 422

XX FT Modified-site 422

XX FT Modified-site 422

XX FT Modified-site 422

XX FT Modified-site 422

XX FT Modified-site 422

XX FT Modified-site 422

XX FT Modified-site 422

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XX FT Modified-site 422

CC also provides a method of identifying a compound that modulates the
 CC activity of SGK. Such compounds are useful for treating patients
 CC requiring modulation of SGK, such as patients with cancer, diabetes
 CC or ischaemic disease.

XX Sequence 431 AA;

Query Match 91.5%; Score 2141; DB 21; Length 431;
 Best Local Similarity 99.3%; Pred. No. 4.7e-191;
 Matches 404; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 39 LAFMKQRRMGLNDFIQKIANNYSACKHPEVQSILKISQPOPELMNANSPPPSPSQOIN 98
 :|||||
 Db 25 IAFMKQRRMGLNDFIQKIANNYSACKHPEVQSILKISQPOPELMNANSPPPSPSQOIN 84
 :|||||

QY 99 LQFSSNPHAKPSDFHFLKVIKGSFGKVLARHKAEEVFYAVKLOKKAILEKKEKHIM 158
 :|||||
 Db 85 LQFSSNPHAKPSDFHFLKVIKGSFGKVLARHKAEEVFYAVKLOKKAILEKKEKHIM 144
 :|||||

QY 159 SERNVLLKNVKHPFLVGLHFSFQTADKLYFVLVDYINGGELFYHLQERCFLEPRARFYAA 218
 :|||||
 Db 145 SERNVLLKNVKHPFLVGLHFSFQTADKLYFVLVDYINGGELFYHLQERCFLEPRARFYAA 204
 :|||||

QY 219 EIASALGYLHSLNIVYRDLKPENILDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 278
 :|||||
 Db 205 EIASALGYLHSLNIVYRDLKPENILDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 264
 :|||||

QY 279 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKLQKLPNTNSA 338
 :|||||
 Db 265 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKLQKLPNTNSA 324
 :|||||

QY 339 RHLLEGLLOKDRTKRLGAKDDFMEIKSHVFFSLINWDDLINCKITPPFPNVSGPNDLRH 398
 :|||||
 Db 325 RHLLEGLLOKDRTKRLGAKDDFMEIKSHVFFSLINWDDLINCKITPPFPNVSGPNDLRH 384
 :|||||

QY 399 FDPEFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLGFSYAPPTDSFL 445
 :|||||
 Db 385 FDPEFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLGFSYAPPTDSFL 431
 :|||||

RESULT 7

AAB24116

ID AAB24116 standard; Protein; 431 AA.

XX AAB24116;

AC AAB24116;

DT 29-JAN-2001 (first entry)

XX Rat serum and glucocorticoid regulated kinase protein (RSGK).

XX Human; STK3; serine threonine kinase; HSGK; RSGK;

XX serum and glucocorticoid regulated kinase.

XX Rattus sp.

XX CN1259573-A.

XX 12-JUL-2000.

XX 29-OCT-1998; 98CN-0123822.

XX 29-OCT-1998; 98CN-0123822.

XX (UYFU-) UNIV FUDAN.

XX Yu L, Fu Q, Zhao Y;

XX WPI; 2000-587991/56.

XX New human serine threonine protein kinase, its code sequence,

XX preparation, and use -

XX Example 3; Fig 4; 29pp; Chinese.

XX

CC The present invention describes human serine threonine kinase STK3,
 CC which is a new member of the serine/threonine protein kinase family.
 CC Human STK3 shares homology with human serum and glucocorticoid
 CC regulated kinase (HSGK) and rat SGK (RSGK). The present sequence
 CC represents the rat RSGK protein sequence from the present invention.

XX Sequence 431 AA;

Query Match 90.5%; Score 2118; DB 21; Length 431;
 Best Local Similarity 97.3%; Pred. No. 6.6e-189;
 Matches 396; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 39 LAFMKQRRMGLNDFIQKIANNYSACKHPEVQSILKISQPOPELMNANSPPPSPSQOIN 98
 :|||||
 Db 25 IAFMKQRRMGLNDFIQKIANNYSACKHPEVQSILKISQPOPELMNANSPPPSPSQOIN 84
 :|||||

QY 99 LQFSSNPHAKPSDFHFLKVIKGSFGKVLARHKAEEVFYAVKLOKKAILEKKEKHIM 158
 :|||||
 Db 85 LQFSSNPHAKPSDFHFLKVIKGSFGKVLARHKAEEVFYAVKLOKKAILEKKEKHIM 144
 :|||||

QY 159 SERNVLLKNVKHPFLVGLHFSFQTADKLYFVLVDYINGGELFYHLQERCFLEPRARFYAA 218
 :|||||
 Db 145 SERNVLLKNVKHPFLVGLHFSFQTADKLYFVLVDYINGGELFYHLQERCFLEPRARFYAA 204
 :|||||

QY 219 EIASALGYLHSLNIVYRDLKPENILDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 278
 :|||||
 Db 205 EIASALGYLHSLNIVYRDLKPENILDSQGHIVLTDGFLCKENIEHNSTTSTFCGTPEYL 264
 :|||||

QY 279 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKLQKLPNTNSA 338
 :|||||
 Db 265 APEVLHKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKLQKLPNTNSA 324
 :|||||

QY 339 RHLLEGLLOKDRTKRLGAKDDFMEIKSHVFFSLINWDDLINCKITPPFPNVSGPNDLRH 398
 :|||||
 Db 325 RHLLEGLLOKDRTKRLGAKDDFMEIKSHVFFSLINWDDLINCKITPPFPNVSGPNDLRH 384
 :|||||

QY 399 FDPEFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLGFSYAPPTDSFL 445
 :|||||
 Db 385 FDPEFTEEPVNSIGKSPDSVLVTASVKEAAEAFGLGFSYAPPTDSFL 431
 :|||||

RESULT 8

AAY93530

ID AAY93530 standard; Protein; 431 AA.

XX AAY93530;

AC AAY93530;

DT 25-SEP-2000 (first entry)

XX A rat serum and glucocorticoid induced protein kinase.

XX Protein kinase; Pkh1; Pkh2; Ypk1; Yrk2; protein kinase B-alpha;

XX serum and glucocorticoid induced protein kinase; SGK; PKBalpha;

XX 3-phosphoinositide-dependent protein kinase-1; PKI; fungal infection;

XX thrush; cancer; diabetes; obesity; antifungal; Candida infection.

XX Rattus sp.

XX WO200036135-A2.

XX 22-JUN-2000.

XX 14-DEC-1999; 99WO-GB04228.

XX 14-DEC-1998; 98US-0112114.

XX (MEDI-) MEDICAL RES COUNCIL.

XX (REGC) UNIV CALIFORNIA.

XX Thorner JW, Alessi DR, Torrance PD, Casamayor A;

XX WPI; 2000-442391/38.

Qy 377 LINKITPPNPNVSGNDLRHFDPEETPEVPNSIGKSPDSVLVTASVKEAAEAFILGFS 436
Db 362 LINKITPPNPNVSGPSDLRHFDPETPEVPSPSSIGRSPDSILVTASVKEAAEAFILGFS 421
Qy 437 YAPPTDSFL 445
Db 422 YAPPVDSFL 430

RESULT 10
AAY48573
ID AAY48573 standard; Protein; 388 AA.
AC AAY48573;
XX
XX 08-DEC-1999 (first entry)
XX Human breast tumour-associated protein 34.
DE
XX Expressed sequence tag; EST; human; breast; cancer; gene therapy;
KW treatment; tumour; cytostatic; medicament.
XX
XX Homo sapiens.
XX
XX DE19813839-A1.
XX
XX 23-SEP-1999.
XX
XX 20-MAR-1998; 98DE-1013839.
XX
XX 20-MAR-1998; 98DE-1013839.
XX
XX (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
XX Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
PI
XX WPI; 1999-528981/45.
DR N-PSDB; AAZ33647.
XX
XX Human nucleic acid sequences and protein products from tumor breast
PT tissue, useful for breast cancer therapy -
PT
XX Claim 22; 157-158; 188pp; German.
XX
XX This invention describes novel human nucleic acid sequences from tumor
CC breast tissue which have cytostatic activity. The nucleic acid sequences
CC can be used to produce and isolate full-length gene sequences. They can
CC be used to express proteins, which can be used as tools to find an
CC activity against breast cancer. The sequences can be used in sense or
CC antisense form. They are especially useful for medicaments for gene
CC therapy to treat breast cancer. AAY48540-Y48617 represent protein
CC fragments encoded by the expressed sequence tags described in the method
CC of the invention.
XX
SQ Sequence 388 AA;

Query Match 85.1%; Score 1992; DB 20; Length 388;
Best Local Similarity 99.2%; Pred No. 3.3e-177;
Matches 377; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 66 PEVQSILKISQBPPELMNPNPSPSPSQOINLGPSNPHAKPSDFHFLKVGKSGFGK 125
Db 9 PEVQSILKISQBPPELMNPNPSPSPSQOINLGPSNPHAKPSDFHFLKVGKSGFGK 68
Qy 126 VLLARHKAEEVFYAVKVLQKAILKKEEKHIMSERVLLKNVGHPELVGLHFSQTADK 185
Db 69 VLLARHKAEEVFYAVKVLQKAILKKEEKHIMSERVLLKNVGHPELVGLHFSQTADK 128
Qy 186 LYFVLDYINGELFYHLQRECFLEPRARFYAAETIASALGYLHSLNIVYRDLKPENILLD 245
Db 129 LYFVLDYINGELFYHLQRECFLEPRARFYAAETIASALGYLHSLNIVYRDLKPENILLD 188

Qy 246 SQGHIVLTDFGLCKENIEHNSTSTFCGTPEYLAPEVLHROPYDRTVDMWCLGAVLYEML 305
Db 189 SQGHIVLTDFGLCKENIEHNSTSTFCGTPEYLAPEVLHROPYDRTVDMWCLGAVLYEML 248
Qy 306 YGLPPPFYSRNTAEYDNLNKLQLEKPNITNSARHLLLEGLLOKDRTKRLGAKDDFMEIKS 365
Db 249 YGLPPPFYSRNTAEYDNLNKLQLEKPNITNSARHLLLEGLLOKDRTKRLGAKDDFMEIKS 308
Qy 366 HVFFSLINWDDLINKKITPPNPNVSGNDLRHFDPEETPEVPNSIGKSPDSVLVTASV 425
Db 309 HVFFSLINWDDLINKKITPPNPNVSGNDLRHFDPEETPEVPNSIGKSPDSVLVTASV 368
Qy 426 KEAAEAFILGFSYAPPTDSFL 445
Db 369 KEAAEAFILGFSYAPPTDSFL 388

RESULT 11
AAB99815
ID AAB99815 standard; Protein; 373 AA.
XX
XX AAB99815;
XX
XX 20-SEP-2001 (first entry)
XX AGC protein kinase family member SGK protein sequence.
XX
XX Protein kinase; identification; hydrophobic pocket; interacting;
KW cancer; diabetes; inhibition; apoptosis; tissue injury;
KW ischaemic injury; stroke.
XX
XX Homo sapiens.
OS
OS Synthetic.
XX
XX WO200144497-A2.
XX
XX 21-JUN-2001.
XX
XX 04-DEC-2000; 2000WO-GB04598.
XX
XX 02-DEC-1999; 99US-0168559.
XX
XX (UYDU-) UNIV DUNDEE.
XX
XX Alessi D, Biondi R;
PI
XX WPI; 2001-390252/41.
XX
XX Identifying modulators of protein kinase (PK) activity, useful in
PT developing drugs for treating cancer or diabetes, by measuring the
PT ability of the compound to modulate or mimic the interaction of PK with
PT interacting polypeptides -
XX
XX Disclosure; Fig 15; 180pp; English.
XX
XX The present invention describes a method for identifying a compound that
CC modulates protein kinase activity. The method comprises measuring the
CC ability of the compound to inhibit, promote or mimic the interaction of
CC a hydrophobic pocket-containing protein kinase with an interacting
CC polypeptide. The interacting polypeptide interacts with the hydrophobic
CC pocket of the protein kinase and/or comprises the amino acid sequence
CC Phe/Tyr-Xaa-Xaa-Phe/Tyr (I). The method is useful in screening assays
CC for developing pharmaceutical compounds or drugs. Compounds, polypeptides
CC or polynucleotides from the present invention are useful in medicine,
CC particularly in the manufacture of a medicament for treating a patient
CC in need of modulation of signalling by a hydrophobic pocket-containing
CC protein kinase. Specifically, the patient has cancer or diabetes or is
CC in need of inhibition of apoptosis, e.g. a patient suffering from tissue
CC injury or ischaemic injury, including stroke. The compound or
CC composition is also useful for inhibiting the degree or rate of
CC phosphorylation by the protein kinase. The interacting polypeptide or
CC compound is useful in methods of stabilising a hydrophobic pocket-
CC containing protein kinase, where the protein kinase is exposed to the

CC compound or polypeptide. AAB99786 to AAB99847 represent amino acid
 CC sequences, and AAH44210 and AAH44211 represent oligonucleotide sequences,
 CC used in the exemplification of the present invention.

XX
 SQ Sequence 373 AA;
 Query Match 84.4%; Score 1976; DB 22; Length 373;
 Best Local Similarity 99.7%; Pred. No. 9.7e-176;
 Matches 372; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 73 KISQBPPELMNANPSPSPSQINLGPSNPHAKPSDFHLKVIKGSFGKVLARHK 132
 DB 1 KISQBPPELMNANPSPSPSQINLGPSNPHAKPSDFHLKVIKGSFGKVLARHK 60
 QY 133 AEEVFYAVKVLQKAILKKKEEKHIMSERVLLKNVHPFLVGLHFSQFADKLYFVLDY 192
 DB 61 AEEVFYAVKVLQKAILKKKEEKHIMSERVLLKNVHPFLVGLHFSQFADKLYFVLDY 120
 QY 193 INGGLFYHLQRECFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHIVL 252
 DB 121 INGGLFYHLQRECFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHIVL 180
 QY 253 TDFGLCKENIEHNSTTSTFCGTPEYLAPEVLHKQPYDRTDWMCLGAVLYEMLYGLPPFY 312
 DB 181 TDFGLCKENIEHNSTTSTFCGTPEYLAPEVLHKQPYDRTDWMCLGAVLYEMLYGLPPFY 240
 QY 313 SRNTAEYDNLNKPQLQKPNITNSARHLLEGLLQKQDRTKRLGAKODFMEIKSHVPSLI 372
 DB 241 SRNTAEYDNLNKPQLQKPNITNSARHLLEGLLQKQDRTKRLGAKODFMEIKSHVPSLI 300
 QY 373 NWDDLINLKITPPPNPNVSGPNDLRHFDPEFTPEPVPNSIGKSPDSVLVTASVKEAAEAF 432
 DB 301 NWDDLINLKITPPPNPNVSGPNDLRHFDPEFTPEPVPNSIGKSPDSVLVTASVKEAAEAF 360
 QY 433 LGFSYAPPTDSFL 445
 DB 361 LGFSYAPPTDSFL 373

RESULT 12
 AAB99836
 ID AAB99836 standard; Protein; 321 AA.
 AC AAB99836;
 XX 20-SEP-2001 (first entry)
 DT AGC protein kinase family member SGK1 protein sequence.
 DE Protein kinase; identification; hydrophobic pocket; interacting;
 KW cancer; diabetes; inhibition; apoptosis; tissue injury;
 KW ischaemic injury; stroke.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200144497-A2.
 XX 21-JUN-2001.
 XX 04-DEC-2000; 2000WO-GB04598.
 XX 02-DEC-1999; 99US-0168559.
 XX (UYDU-) UNIV DUNDEE.
 XX Alessi D, Biondi R;
 XX WPI; 2001-390252/41.
 XX Identifying modulators of protein kinase (PK) activity, useful in
 PT developing drugs for treating cancer or diabetes, by measuring the
 PT ability of the compound to modulate or mimic the interaction of PK with

PT interacting polypeptides -
 XX Disclosure; Fig 16; 180pp; English.

XX
 CC The present invention describes a method for identifying a compound that
 CC modulates protein kinase activity. The method comprises measuring the
 CC ability of the compound to inhibit, promote or mimic the interaction of
 CC a hydrophobic pocket-containing protein kinase with an interacting
 CC polypeptide. The interacting polypeptide interacts with the hydrophobic
 CC pocket of the protein kinase and/or comprises the amino acid sequence
 CC Phe/Tyr-Xaa-Xaa-Phe/Tyr (I). The method is useful in screening assays
 CC for developing pharmaceutical compounds or drugs. Compounds, polypeptides
 CC or polynucleotides from the present invention are useful in medicine,
 CC particularly in the manufacture of a medicament for treating a patient
 CC in need of modulation of signalling by a hydrophobic pocket-containing
 CC protein kinase. Specifically, the patient has cancer or diabetes or is
 CC in need of inhibition of apoptosis, e.g. a patient suffering from tissue
 CC injury or ischaemic injury, including stroke. The compound or
 CC composition is also useful for inhibiting the degree or rate of
 CC phosphorylation by the protein kinase. The interacting polypeptide or
 CC compound is useful in methods of stabilising a hydrophobic pocket-
 CC containing protein kinase, where the protein kinase is exposed to the
 CC compound or polypeptide. AAB99786 to AAB99847 represent amino acid
 CC sequences, and AAH44210 and AAH44211 represent oligonucleotide sequences,
 CC used in the exemplification of the present invention.

XX Sequence 321 AA;

Query Match 72.6%; Score 1699; DB 22; Length 321;
 Best Local Similarity 100.0%; Pred. No. 5.7e-150;
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 125 KVLARHKAEEVFYAVKVLQKAILKKKEEKHIMSERVLLKNVHPFLVGLHFSQFAD 184
 DB 1 KVLARHKAEEVFYAVKVLQKAILKKKEEKHIMSERVLLKNVHPFLVGLHFSQFAD 60
 QY 185 KLYFVDYINGGELFYHLQRECFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILL 244
 DB 61 KLYFVDYINGGELFYHLQRECFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILL 120
 QY 245 DSQGHIVLTDGFCCKENIEHNSTTSTFCGTPEYLAPEVLHKQPYDRTDWMCLGAVLYEM 304
 DB 121 DSQGHIVLTDGFCCKENIEHNSTTSTFCGTPEYLAPEVLHKQPYDRTDWMCLGAVLYEM 180
 QY 305 LYGLPPFSYRNTAEYDNLNKPQLQKPNITNSARHLLEGLLQKQDRTKRLGAKODFMEIK 364
 DB 181 LYGLPPFSYRNTAEYDNLNKPQLQKPNITNSARHLLEGLLQKQDRTKRLGAKODFMEIK 240
 QY 365 SHVFFSLINWDDLINLKITPPPNPNVSGPNDLRHFDPEFTPEPVPNSIGKSPDSVLVTAS 424
 DB 241 SHVFFSLINWDDLINLKITPPPNPNVSGPNDLRHFDPEFTPEPVPNSIGKSPDSVLVTAS 300
 QY 425 VKEAAEAFLGFSYAPPTDSFL 445
 DB 301 VKEAAEAFLGFSYAPPTDSFL 321

RESULT 13
 AAB97772
 ID AAB97772 standard; Protein; 496 AA.
 XX AAB97772;
 AC AAB97772;
 XX 17-MAR-1999 (first entry)
 DT Human serum glucocorticoid-regulated kinase (H-SGK2) polypeptide.

XX Serum glucocorticoid-regulated kinase; H-SGK2; human; gene therapy;
 KW serine/threonine protein kinase; inflammation; rheumatoid arthritis;
 KW septicemia; autoimmune disease; inflammatory bowel disease; psoriasis;
 KW transplant rejection; infection; stroke; ischaemia; renal disorder;
 KW restenosis; brain injury; acquired immune deficiency syndrome; AIDS;
 KW metabolic; bone; osteoporosis; lymphoproliferation; atherosclerosis;

KW Alzheimer's disease; cancer.
OS Homo sapiens.
FN EP889127-A1.
XX 07-JAN-1999.
XX 18-JUN-1998; 98EP-0304830.
XX 23-DEC-1997; 97US-0997212.
PR 01-JUL-1997; 97US-0051446.
XX (SMIK) SMITHLINE BEECHAM CORP.
PA Kumar S, Zou C;
PI WPI; 1999-062658/06.
DR N-PSDB; AAV99653.
XX New nucleic acid encoding human H-SGK2 poly-peptide(s) - useful for
PT diagnosis, treatment and prevention of e.g. arthritis, infections,
PT cancer, Alzheimer's disease
XX Claim 11; Page 8; 27pp; English.
PS
XX This represents a human serum glucocorticoid-regulated kinase (H-SGK2)
CC polypeptide, a novel member of the serine/threonine protein kinase
CC family. A host cell transfected or transformed with an expression system
CC comprising the H-SGK2 nucleic acid can be used for the recombinant
CC production of the protein. The H-SGK2 polypeptide is useful for treating
CC a subject who require enhanced/reduced activity or expression/inhibition
CC of the polypeptide. Recombinant H-SGK2 is used to raise antibodies; in
CC vaccines; in drug screens; and to identify soluble or membrane-bound
CC receptors. The H-SGK2 polypeptides are useful for treating inflammation
CC (rheumatoid arthritis); septicemia; autoimmune disease (inflammatory
CC bowel disease or psoriasis); transplant rejection; infection; stroke;
CC ischaemia; renal disorders; restenosis; brain injury; acquired immune
CC deficiency syndrome; metabolic and other bone diseases (osteoporosis);
CC cancer (e.g. lymphoproliferation); atherosclerosis and Alzheimer's
CC disease. The H-SGK2 nucleic acids can be used in gene therapy.
XX
SQ Sequence 496 AA;
Query Match 63.3%; Score 1481; DB 20; Length 496;
Best Local Similarity 67.7%; Pred. No. 2.4e-129;
Matches 281; Conservative 52; Mismatches 68; Indels 14; Gaps 3;
Qy 41 FMKORRMGLNDFIQKIANNYSACKHPEVQSILKISQPEPELMNANSPPPP----- 91
Db 86 FIKORRAGLNEFIQNLVRYPELYKHPDVRAPLQMDSPKH----QSDPSEDEDERSSQKLH 141
Qy 92 SPSQOINLGSPSSNPHAKPSDFHLKVGSGFGKVLARHKAEEVFYAVKVLQKAILKK 151
Db 142 STSQINILGSGNPHAKPTDFDKVLKVGSGFGKVLAKRDLGKFYAVKVLQKIVLNR 201
Qy 152 KEKHIMSRNVLKXKHPFLVGLHFSFQTADKLYFVLDYINGGELFYHLQRCFLEP 211
Db 202 KEQKHAERNVLLKNVHPFLVGLHFSFQTTEKLYFVLDVNGGELFYHLQRCFLEP 261
Qy 212 RARFYAEIASALGYLSHNLNIVYRDLPENILDSQGHVLTDFGLCKENIENHSTTTF 271
Db 262 RARFYAEIASALGYLSHNLNIVYRDLPENILDSVGHVLTDFGLCKEGIAISDTTTF 321
Qy 272 CGTPEYLAPVLLHQPDRYTDVWCLGAVLYEMLYGLPPFYSRTAEMYNILNKPLOLK 331
Db 322 CGTPEYLAPVIRKQPDYTDVWCLGAVLYEMLYGLPPFYCRDVAEMYNILNKPLOLSR 381
Qy 332 PNTNSARHLLEGILQKDRKRLGAKDDFMEIKSHVFFSLINDDLNKKITPPENPNVS 391
Db 382 PGVSLTAWSLTEELLELEKDRQNLGAKEDFLEIQNHPPFESLSWADLVQKKIPPPFNVA 441
Qy 392 GPNDLRHDFEPTTEPVNSIGKSPDSVLVTASVKEAAEAFLGFSYAPPT--DSFL 445

Db 442 GPDIRNFDTAFTETVPYSCVSSDYIVNASVLEADDAFVGFSYAPPSDELFL 496
RESULT 14
AAAY95278
ID AAY95278 standard; Protein; 429 AA.
XX AC AAY95278;
XX 12-SEP-2000 (first entry)
XX Human serum and glucocorticoid-induced protein kinase 3.
XX Serum and glucocorticoid-induced protein kinase 3; SGK3;
XX human; phosphorylation; cancer; diabetes; ischaemia; therapy.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Modified-site 77
FT /note= "O-phosphorylated"
FT Modified-site 79
FT /note= "O-phosphorylated"
XX WO200035946-A1.
XX 22-JUN-2000.
XX 14-DEC-1999; 99WO-GB04232.
XX 14-DEC-1998; 98US-0112217.
PR 19-AUG-1999; 99GB-0019676.
XX (UYDU-) UNIV DUNDEE.
XX Cohen P, Kobayashi T, Deak M;
XX WPI; 2000-442364/38.
DR N-PSDB; AAA27858.
XX Modulation of serum and glucocorticoid-induced protein kinase (SGK) by
PT phosphorylation with 3-phosphoinositide-dependent protein kinase-1
PT (PDK1) or dephosphorylation, useful for treatment of cancer, diabetes
PT and ischemic diseases -
XX Disclosure; Page 7; 127pp; English.
XX The present sequence is that of human serum and
CC glucocorticoid-induced protein kinase (SGK) isoform 3. SGK
CC (see AAY95279) was initially identified as a glucocorticoid and
CC osmotic stress-responsive gene. SGK3 is activated by
CC phosphorylation in a similar manner to SGK. The invention provides
CC methods of activating SGK activity by phosphorylation using
CC 3-phosphoinositide-dependent protein kinase-1 (PDK1), and of
CC reducing the activity of SGK by dephosphorylation. The invention
CC also provides a method of identifying a compound that modulates the
CC activity of SGK. Such compounds are useful for treating patients
CC requiring modulation of SGK, such as patients with cancer, diabetes
CC or ischaemic disease.
XX
SQ Sequence 429 AA;
Query Match 63.1%; Score 1476; DB 21; Length 429;
Best Local Similarity 67.5%; Pred. No. 5.7e-129;
Matches 280; Conservative 52; Mismatches 69; Indels 14; Gaps 3;
Qy 41 FMKORRMGLNDFIQKIANNYSACKHPEVQSILKISQPEPELMNANSPPPP----- 91
Db 19 FIKORRAGLNEFIQNLVRYPELYKHPDVRAPLQMDSPKH----QSDPSEDEDERSSQKLH 74
Qy 92 SPSQOINLGSPSSNPHAKPSDFHLKVGSGFGKVLARHKAEEVFYAVKVLQKAILKK 151

Db 75 STSONINLPGSNPHAKPTDFDLKVIKGSFGKVLAKRKLKDGKVFYKVLQKIVLNR 134
Qy 152 KEEKHINSERNVLLKNVHPFLVGLHESFQADKLYEVLDYINGGELFYHLORECFLEP 211
Db 135 KEQKHINAERNVLLKNVHPFLVGLHYFSQTEKLYEVLDVANGGELFFHLORESFPEH 194
Qy 212 RARFYAAEIASALGYLSHSLNIVYRDLPENILDSQGHIVLTFGLCKENIEHNSSTTF 271
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Qy 272 CGTPEYLAPEVLHKQPDYRTVDMWCLGAVLYEMLYGLPPFYSRNTAEMYNILNKPQLK 331
Db 255 CGTPEYLAPEVIRKQPDYNTVDMWCLGAVLYEMLYGLPPFYCRDVAEMYDNILHKPLSLR 314
Qy 332 PNITNSARHLEGLLQKORTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFNPNVS 391
Db 315 PGVSLTAMSLTEELLEKDRQNRGAKEDFLEIQNHPPFESLWADLVQKXIPPPFNPNVA 374
Qy 392 GPDLRHPDFEFTPEEPNPSIGKSPDSVLVTASVKEAAEAFLGFSYAPPT-DSFL 445
Db 375 GPDDIRNFTAFTEETVPYSVCVSSDYSIVNASVLEADDAFVGFSYAPPSDELFL 429

RESULT 15
AAU87228
ID AAU87228 standard; Protein; 496 AA.
AC AAU87228;
XX
DT 05-JUN-2002 (first entry)
XX
DE Novel central nervous system protein #138.
XX
KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy.
XX
OS Homo sapiens.
XX
PN W020015318-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01332.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
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PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
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PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
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PR 05-SEP-2000; 2000US-0229509.
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PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
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PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234423.
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PR 25-SEP-2000; 2000US-0234997.
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PR 27-SEP-2000; 2000US-0235834.
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PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0239937.
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PR 20-OCT-2000; 2000US-0241221.
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PR 08-NOV-2000; 2000US-0246474.
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PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.

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 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-581633/65.

N-PSDB; ABK43558.

New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -

Claim 9; SEQ ID No 746; 837pp; English.

The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease and ankyrotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial

CC infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,

Query Match 63.1%; Score 1476; DB 22; Length 496;
 Best Local Similarity 67.5%; Pred. No. 7.1e-129;
 Matches 280; Conservative 52; Mismatches 69; Indels 14; Gaps 3;
 QY 41 FMKORRMGLNDFIQTANNYSACKHPVEQSILKISQPEPELMNANPSPPP----- 91
 Db 86 FIKORRAGLNEFIQNLVRYPELVNHPDVRAFLQMDSPKH---QSDPSEDEDESSQKLH 141
 QY 92 SPQQINLGPSSNPHAKPSDFELKVIKGSFGKVLARHKAEEVFYAVKVLQKALKK 151
 Db 142 STSQINLGPSCNPHAKPTDFELKVIKGSFGKVLAKRKLQKGFYAVKVLQKIVLNR 201
 QY 152 KEEKHIMSERVILLKNVKGHPFLVGLHPSFQTADKLYFVLDYINGGELFYHLQRCFLEP 211
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 QY 212 RARFYAAETASALGYLHSLNIVYRDLKPENILLDSQGHIVLTFGLCKENIEHNTSTTF 271
 Db 262 RARFYAAETASALGYLHSLNIVYRDLKPENILLDSVGHVVLTFGLCKEGIAISDTTTF 321
 QY 272 CGTPEYLAPVHLKQPYDRTVDMWCLGAVLYEMLYGLPPFYSRNTAEYDNIILNKPLQLK 331
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 QY 332 PNITNSARHLLEGGLQKRTKRLGAKDDFMEIKSHVFFSLINWDDLINKKITPPFPNPVS 391
 Db 382 PGVSLTAWSLIEELLEKDRQNLGAKEDFLEIQNHPPFESLSWADLVQKKIPPEFNVA 441
 QY 392 GPNDLRHFDPEFTEEPVPSIGKSPSVLVTASVKEAAEAFGFSYAPPT-DSFL 445
 Db 442 GPDDIRNFDTAFTETVPYSCVSDYSIVNASVLEADDAFVGFSYAPPSDEDLFL 496

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